

From: Li, Ruixiang
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CH

Searcher: D. Schreiber
Phone: 308-4292
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Date Picked Up: 6/13
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Searcher Prep/Review: 7
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TYPE OF SEARCH:
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AA Sequences: 3
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: Cambridge
WWW/Internet: _____
Other (specify): _____

A;Residues: 98-125 <SP>
 R; Andrews, P.C.; Nichols, R.; Dixon, J.E.
 J. Biol. Chem. 262, 12692-12699, 1987
 A;Title: Post-translational processing of preprosomatostatin-II examined using fast atom
 A;Reference number: A27376; MUID:87308304
 A;Accession: A27376
 A;Molecule type: protein
 A;Residues: 1-76, DV, 79-89, 'G', 91-125 <AND>
 C;Superfamily: somatostatin
 C;Keywords: hydroxylsine; neuropeptide; pyroglutamic acid
 F;1-24/Domain: propeptide #status experimental <PRO>
 F;97-125/Product: somatostatin II #status experimental <MAT>
 F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
 F;114-125/Disulfide bonds: #status experimental
 F;120/Modified site: hydroxylsine (Lys) #status experimental

Query Match 32.5%; Score 194; DB 1; Length 125;
 Best Local Similarity 39.3%; Pred. No. 1.9e-13;
 Matches 53; Conservative 11; Mismatches 29; Indels 42; Gaps 6;
 A;Cross-references: GB:J00306; PIDN:AAA60566.1; PID:9338288
 A;Experimental source: Pancreatic somatostatinoma
 R;Shen, L.P.; Boileau, G.; Zollinger, L.; Nault, C.; Rholam, M.; Cohen, P.
 EMBO J. 8, 2911-2916, 1989
 A;Title: Site-specific mutagenesis identifies amino acid residues critical in prohorm
 A;Reference number: S09381; MUID:90059875
 A;Accession: A01430
 A;Molecule type: mRNA
 A;Residues: 1-116 <SH2>
 A;Cross-references: GB:J00306; PIDN:AAA60566.1; PID:9338288
 A;Experimental source: Pancreatic somatostatinoma
 R;Shen, L.P.; Picket, R.L.; Rutter, W.J.
 Proc. Natl. Acad. Sci. U.S.A. 79, 4575-4579, 1982
 A;Title: Human somatostatin I: sequence of the cDNA.
 A;Reference number: A01430; MUID:83014931
 A;Accession: A01430
 A;Molecule type: mRNA
 A;Residues: 1-116 <SH2>
 A;Cross-references: GB:J00306; PIDN:AAA60566.1; PID:9338288
 A;Experimental source: Pancreatic somatostatinoma
 R;Shen, L.P.; Boileau, G.; Zollinger, L.; Nault, C.; Rholam, M.; Cohen, P.
 EMBO J. 8, 2911-2916, 1989
 A;Title: Site-specific mutagenesis identifies amino acid residues critical in prohorm
 A;Reference number: S09381; MUID:90059875
 A;Accession: S09381
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 88-108 <GOM>
 R;Odum, L.; Johnsen, A.H.
 Biochem. J. 303, 263-268, 1994
 A;Title: Human seminal plasma contains somatostatin-64.
 A;Reference number: S50024; MUID:95031969
 A;Accession: S50024
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 53-62, 67-82 <ODU>
 C;Comment: Somatostatin inhibits the release of somatotropin.
 C;Genetics:
 A;Gene: GDB:SSST
 A;Cross-references: GDB:119604; OMIM:182450
 A;Map position: 3q28-3q28
 A;Introns: 46/3
 C;Function:
 A;Description: inhibits the secretion of a number of peptide hormones, including soma
 C;Superfamily: somatostatin
 C;Keywords: hormone; hypothalamus; neuropeptide
 F;1-24/Domain: signal sequence #status Predicted <SIG>
 F;25-88/Domain: propeptide #status Predicted <PRO>
 F;89-116/Product: somatostatin-28 #status Predicted <PRO>
 F;103-116/Product: somatostatin-14 #status Predicted <PRO>
 F;110-116/Disulfide bonds: #status Predicted

RESULT 3

S20630 somatostatin precursor - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
 C;Accession: S20630
 R;Nata, K.; Kobayashi, T.; Karahashi, K.; Kato, S.; Yamamoto, H.; Yonékiura, H.; Okamoto,
 submitted to the EMBL Data Library, June 1991
 A;Description: Nucleotide sequence determination of chicken somatostatin precursor cDNA.
 A;Reference number: S20630
 A;Accession: S20630
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-116 <NAT>
 C;Cross-references: EMBL:X60191; PIDN:962985; PID:962986
 C;Superfamily: somatostatin

Query Match 30.1%; Score 179.5; DB 1; Length 116;

Best Local Similarity 39.8%; Pred. No. 6.2e-12;

Matches 49; Conservative 20; Mismatches 27; Indels 27; Gaps 6;

Query Match 29.6%; Score 176.5; DB 1; Length 116;

Best Local Similarity 38.2%; Pred. No. 1.3e-11;

Matches 47; Conservative 19; Mismatches 30; Indels 27; Gaps 6;

Query 5 QIHCALALGLALICSQGAA-SQPDLDLQLRALLAALPHRGSGVSEWRRTFYPNC 63

DB 5 RLQCALALLSIALAVGTVSAAPSQDPLR---RQFLQKSLAA---AGKQELAKYFLAE- 55

Query 64 PCLRWRPRKVKGPQLKAKE-----DLERSVDNLPL---PRERKAGCKNEYWKGF 108

DB 56 -LLSEPSOTENEALESEDLSRGAEQDEVRJELERSANSNPALAPRERKAGCKNEYWKTF 113

Query 109 TSC 111

DB 114 TSC 116

RESULT 4
 RIHUS1 somatostatin I precursor - human

RESULT 5

Qy	60	YPNCPCCLRWRPRKVKGPKLAKKE- somatostatin I precursor - crab-eating macaque N;Alternate names: preprosomatostatin N;Contains: somatostatin 14 (SS-14); somatostatin 28 (SS-28) C;Species: Macaca fascicularis (crab-eating macaque) C;Date: 30-Jun-1989 #sequence_revision 31-Jan-1997 #text_change 18-Jun-1999 C;Accession: A28968	DLERSVDNLPP--PRERKAGCKNEY 104
Db	52	LAE--LLSEPSQTDNNEALESDDLPRGAEQDEVRLERSANSSPALPRERKAGCKNEY 108	
Qy	105	WKGFTSC 111	
Db	109	WKTFTSC 115	
RESULT 7			
RIRTS1			
somatostatin precursor - rat			
N;Alternate names: preprosomatostatin			
N;Contains: somatostatin-14; somatostatin-28			
C;Species: Rattus norvegicus (Norway rat)			
C;Comment: Somatostatin inhibits the release of somatotropin.			
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 18-Jun-1999			
C;Accession: A20983; A01431; A47598; A22529; 155220; 151829			
R;Montminy, M.R.; Goodman, R.H.; Horovitch, S.J.; Habener, J.F.			
Proc. Natl. Acad. Sci. U.S.A. 81, 3337-3340, 1984			
F;1-24;/Domain: signal sequence #status predicted <SIG>			
F;25-88;/Domain: propeptide #status predicted <PRO>			
F;89-116/Product: somatostatin-28 #status predicted <M28>			
F;103-116/Product: somatostatin-14 #status predicted <M14>			
F;105-116/Disulfide bonds: #status predicted			
A;Accession: A20983			
A;Molecule type: DNA			
A;Residues: 1-116 <MON>			
A;Cross-references: GB:J00787; NID:9207024; PIDN:AAA42164.1; PID:9207025			
A;Note: the authors translated the codon ACC for residue 43 as Tyr			
R;Argos, P.; Taylor, W.L.; Minth, C.D.; Dixon, J.E.			
J. Biol. Chem. 258, 8788-8793, 1983.			
A;Title: Primary structure of the gene encoding rat preprosomatostatin.			
A;Reference number: A20983; MUID:84221954			
A;Accession: A20983			
A;Molecule type: DNA			
A;Residues: 1-116 <MON>			
A;Cross-references: GB:J00787; NID:9207024; PIDN:AAA42164.1; PID:9207025			
A;Note: the authors translated the codon ACC for residue 43 as Tyr			
R;Argos, P.; Taylor, W.L.; Minth, C.D.; Dixon, J.E.			
J. Biol. Chem. 258, 8788-8793, 1983.			
A;Title: Nucleotide and amino acid sequence comparisons of preprosomatostatin			
A;Reference number: A01431; MUID:83238516			
A;Accession: A01431			
A;Status: nucleic acid sequence not shown			
A;Molecule type: mRNA			
A;Residues: 1-116 <ARG>			
R;Benoit, R.; Ling, N.; Esch, F.			
Science 238, 1126-1129, 1987.			
A;Title: A new prosomatostatin-derived peptide reveals a pattern for prohormone processing			
A;Reference number: A47598; MUID:88070564			
A;Accession: A47598			
A;Status: preliminary			
A;Molecule type: protein			
A;Residues: 25-34 <BEEN>			
R;Tavianini, M.A.; Hayes, T.E.; Magazin, M.D.; Dixon, J.E.			
J. Biol. Chem. 259, 11798-11803, 1984			
A;Title: Isolation, characterization, and DNA sequence of the rat somatostatin gene			
A;Reference number: A22529; MUID:85006903			
A;Accession: A22529			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-116 <TAV>			
R;Benoit, R.; Ling, N.; Esch, F.			
Science 238, 1126-1129, 1987.			
A;Title: A new prosomatostatin-derived peptide reveals a pattern for prohormone processing			
A;Reference number: A47598; MUID:88070564			
A;Accession: A47598			
A;Status: preliminary			
A;Molecule type: protein			
A;Residues: 25-34 <BEEN>			
R;Tavianini, M.A.; Hayes, T.E.; Magazin, M.D.; Dixon, J.E.			
J. Biol. Chem. 259, 11798-11803, 1984			
A;Title: Isolation, characterization, and DNA sequence of the rat somatostatin gene			
A;Reference number: A22529; MUID:85006903			
A;Accession: A22529			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-116 <TAV>			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
C;Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.			
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
C;Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.			
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
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C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
C;Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.			
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
C;Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.			
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
C;Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.			
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
C;Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.			
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
C;Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.			
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
C;Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.			
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
C;Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.			
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			
C;Species: Rana ridibunda (laughing frog)			
C;Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.			
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999			
C;Accession: JC6166			
R;Tostivint, H.; Lihirman, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; C.;Accession: JC6166			

A;Description: inhibits the secretion of a number of peptide hormones, including somatotropin
 C;Superfamily: somatostatin
 C;Keywords: hormone; hypothalamus; neuropeptide
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-88/Domain: propeptide #status experimental <PRO>
 F;89-116/Product: somatostatin-28 #status predicted <S28>
 F;103-116/Product: somatostatin-28 #status predicted <S14>
 F;105-116/Disulfide bonds: #status predicted

Query Match 27.4%; Score 163.5; DB 1; Length 116;
 Best Local Similarity 37.4%; Pred. No. 3.1e-10;
 Matches 46; Conservative 19; Mismatches 31; Indels 27; Gaps 6;
 Qy 5 QIHCALALLGLALAICS-QGAASQPDLLASRRLLQRALAAALPHRGSGVSERWRTFYPNC 63
 Db 5 RLOCALAALCIVALGGVTGAPSQDPRL---RQFLQSKLAAA---TGKQELAKYFLAE- 55
 Qy 64 PCLRWWRPKVKGPKLAKAE-----DLERSVDNLP---PRERKAGCKNFKYWKGF 108
 Db 56 -LLSEPNOTENDALEPEDLPQAAEQDEMRLQSRANSNPAMAPRERKAGCKNFKYWKGF 113
 Qy 109 TSC 111
 Db 114 TSC 116

RESULT 8 RIMSS1
 somatostatin precursor - mouse.
 N;Alternate names: preprosomatostatin
 N;Contains: somatostatin 14 (SS-14); somatostatin 28 (SS-28)
 C;Species: Mus musculus (house mouse)
 C;Accession: S08416
 R;Fuhrmann, G.; Heilig, R.; Kempf, J.; Ebel, A.
 Nucleic Acids Res. 18, 1287, 1990
 A;Title: Nucleotide sequence of the mouse preprosomatostatin gene.
 A;Reference number: S08416; MUID:90206793
 A;Molecule type: DNA
 A;Residues: 1-116 <FUH>
 A;Cross-references: EMBL:X51468; NID:953768; PIDN:CAA35831.1; PID:9297530
 C;Comment: Somatostatin inhibits the release of somatotropin.
 C;Genetics:
 A;Introns: 46/3
 C;Superfamily: somatostatin
 C;Keywords: hormone; neuropeptide
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-88/Domain: propeptide #status predicted <PRO>
 F;89-116/Product: somatostatin-28 #status predicted <S28>
 F;103-116/Product: somatostatin-14 #status predicted <S14>
 F;105-116/Disulfide bonds: #status predicted

Query Match 27.4%; Score 163.5; DB 1; Length 116;
 Best Local Similarity 37.4%; Pred. No. 4e-10;
 Matches 46; Conservative 19; Mismatches 31; Indels 27; Gaps 6;
 Qy 5 QIHCALALLGLALAICS-QGAASQPDLLASRRLLQRALAAALPHRGSGVSERWRTFYPNC 63
 Db 5 RLOCALAALCIVALGGVTGAPSQDPRL---RQFLQSKLAAA---AGKQELAKYFLAE- 55
 Qy 64 PCLRWWRPKVKGPKLAKAE-----DLERSVDNLP---PRERKAGCKNFKYWKGF 108
 Db 56 -LLSEPNOTENDALEPEDLPQAAEQDEMRLQSRANSNPAMAPRERKAGCKNFKYWKGF 113
 Qy 109 TSC 111
 Db 114 TSC 116

RESULT 10 RIIDS1
 somatostatin-14 precursor - channel catfish
 N;Alternate names: somatostatin I
 N;Contains: somatostatin-14
 C;Species: Ictalurus punctatus (channel catfish)
 C;Accession: S00292; #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
 R;Minth, C.D.; Taylor, W.L.; Magazin, M.; Tavianini, M.A.; Collier, K.; Weith, H.L.; J. Biol. Chem. 257, 10372-10377, 1982
 A;Title: The structure of cloned DNA complementary to catfish pancreatic somatostatin
 A;Reference number: S00292; MUID:82265698
 A;Accession: S00292
 A;Molecule type: mRNA
 A;Residues: 1-14 <MIN>
 A;Cross-references: EMBL:V00607; NID:964017; PIDN:CAA23877.1; PID:964018
 R;Taylor, W.L.; Collier, K.J.; Deschenes, R.J.; Weith, H.L.; Dixon, J.E.
 Proc. Natl. Acad. Sci. U.S.A. 78, 6694-6698, 1981
 A;Title: Sequence analysis of a cDNA coding for a pancreatic precursor to somatostatin
 A;Reference number: A93897; MUID:82082515
 A;Accession: A93897
 A;Molecule type: mRNA
 A;Residues: 82-108 <TAY>
 A;Cross-references: GB:J00944
 R;Andrews, P.C.; Dixon, J.E.
 J. Biol. Chem. 256, 8267-8270, 1981
 A;Title: Isolation and structure of a peptide hormone predicted from a mRNA sequence
 A;Reference number: A92334; MUID:81264223
 A;Accession: A92334

RESULT 9

A; Molecule type: protein
 A; Residues: 101-114 <AND>
 C; Superfamily: somatostatin
 C; Keywords: neuropeptide
 F; 1-24/Domain: signal sequence #status predicted <SIG>
 F; 25-100/Domain: propeptide #status predicted <PRO>
 F; 101-114/Product: somatostatin-14 #status experimental <MAT>
 F; 103-114/Disulfide bonds: #status experimental

Query Match 26.2%; Score 156.5; DB 1; Length 114;
 Best Local Similarity 31.4%; Pred. No. 1.7e-09;
 Matches 43; Conservative 20; Mismatches 25; Indels 49; Gaps 5;

Query Match 24.6%; Score 147; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.8e-09;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRVSQIHLALLGLALAICS-QGAASQPDLILASRRILLQRALAAALPHRSQGVSERWRTF 59
 Db 1 MPSTRICQCALALLAVALSVCSVSGAPS---DAKLRLQFLQRSILA-----41

Qy 60 YPNCPCLLRWRPRKVKGPOLAK-----EDLERSYDΝ-----LPPR 94
 Db 42 ---PSTVKQELTRYTLAELLAQAESEGARLEMERAAAGPMLAPR 97

Qy 95 ERKAGCKNFKYWKFTSC 111
 Db 98 ERKAGCKNFKFWKTFSC 114

RESULT 11
 150798 preprosomatostatin SS-14 - channel catfish
 C; Species: Ictalurus punctatus (channel catfish)
 C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C; Accession: 150798
 R; Dixon, J.E.; Andrews, P.C.
 Adv. Exp. Med. Biol. 188, 19-29, 1985
 A; Title: Somatostatin of the channel catfish.
 A; Reference number: 150798; MUID:85303576
 A; Accession: 150798
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: mRNA
 A; Residues: 1-114 <DIX>
 A; Cross-references: GB:255903; NID:9213339; PIDN:AAA49339; PID:9213340
 C; Superfamily: somatostatin

Query Match 26.2%; Score 156.5; DB 2; Length 114;
 Best Local Similarity 31.4%; Pred. No. 1.7e-09;
 Matches 43; Conservative 20; Mismatches 25; Indels 49; Gaps 5;

Query Match 24.6%; Score 147; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.8e-09;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRVSQIHLALLGLALAICS-QGAASQPDLILASRRILLQRALAAALPHRSQGVSERWRTF 59
 Db 1 MPSTRICQCALALLAVALSVCSVSGAPS---DAKLRLQFLQRSILA-----41

Qy 60 YPNCPCLLRWRPRKVKGPOLAK-----EDLERSYDΝ-----LPPR 94
 Db 42 ---PSTVKQELTRYTLAELLAQAESEGARLEMERAAAGPMLAPR 97

Qy 95 ERKAGCKNFKYWKFTSC 111
 Db 98 ERKAGCKNFKFWKTFSC 114

RESULT 12
 A60842 somatostatin-25 - coho salmon
 N; Alternate names: somatostatin II precursor
 C; Species: Oncorhynchus kisutch (coho salmon)
 C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C; Accession: A60842; C60842
 R; Plisetskaya, E.M.; Pollock, H.G.; Rouse, J.B.; Hamilton, J.W.; Kimmel, J.R.; Andrews, Gen. Comp. Endocrinol. 63, 252-263, 1986
 A; Title: Characterization of coho salmon (Oncorhynchus kisutch) islet somatostatins.
 A; Reference number: A60842; MUID:87055212

A; Molecule type: protein
 A; Residues: 1-25 <PLI>
 A; Accession: C60842
 A; Molecule type: protein
 A; Residues: 12-25 <PL2>
 A; Note: this form, somatostatin II, was not sequenced directly, but rather deduced from the N-terminus
 C; Superfamily: somatostatin
 C; Keywords: hormone; pancreatic islet
 F; 1-25/Product: somatostatin-25 #status experimental <MAT1>
 F; 12-25/Product: somatostatin II #status experimental

Query Match 24.6%; Score 147; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.8e-09;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 SVDNLPPRERKAGCKNFKYWKFTSC 111
 Db 1 SVDNLPPRERKAGCKNFKYWKFTSC 25

RESULT 13
 S00169 somatostatin II precursor - European flounder (tentative sequence) (fragments)
 C; Species: Platichthys flesus (European flounder)
 C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Mar-2000
 C; Accession: S00169
 R; Conlon, J.M.; Davis, M.S.; Falkmer, S.; Thim, L.
 Eur. J. Biochem. 168, 647-652, 1987
 A; Title: Structural characterization of peptides derived from prosomatostatins. I and II
 A; Reference number: S00166; MUID:88029486
 A; Accession: S00169
 A; Molecule type: protein
 A; Residues: 1-10;11-45;46-73 <CON>
 A; Note: three peptides which probably originate from a common precursor, were isolated
 C; Superfamily: somatostatin
 C; Keywords: glycoprotein; neuropeptide; pancreatic islet

F; 1-10/Product: peptide F1 #status experimental <PF1>
 F; 11-45/Product: peptide F3 #status experimental <PF3>
 F; 46-73/Product: peptide F2 #status experimental <PF2>
 F; 62-73/Disulfide bonds: #status experimental

Query Match 22.8%; Score 136; DB 2; Length 73;
 Best Local Similarity 51.9%; Pred. No. 1.7e-07;
 Matches 27; Conservative 4; Mismatches 5; Indels 16; Gaps 2;

Qy 76 POLKAKEDLE-----RSVD---NLPPRERKAGCKNFKYWKFTSC 111
 Db 22 PEADQDAEMVSTATGGGRMMQESIEPPNNLPPRERKAGCKNFKYWKFTSC 73

RESULT 14
 RPPGS somatostatin I precursor - pig (fragment)
 N; Alternate names: prossomatostatin 14 (SS-14); somatostatin 28 (SS-28)
 C; Species: Sus scrofa domestica (domestic pig)
 C; Date: 30-Nov-1980 #sequence_revision 31-Jan-1997 #text_change 31-Jan-1997
 C; Accession: A34109; A24222; A91273; A93854; A90398; S13616; A01432
 R; Bersani, M.; Thim, L.; Baldissera, F.G.A.; Holst, J.J.
 J. Biol. Chem. 264, 10633-10636, 1989
 A; Title: Prossomatostatin 1-64 is a major product of somatostatin gene expression in
 A; Reference number: A34109; MUID:89278131
 A; Accession: A34109
 A; Molecule type: protein
 A; Residues: 1-64 <BER>
 R; Schmidt, W.E.; Mutt, V.; Kratzin, H.; Carlquist, M.; Conlon, J.M.; Creutzfeldt, W.
 FEBS Lett. 192, 141-146, 1985
 A; Title: Isolation and characterization of pross1-32, a peptide derived from the N-terminal
 A; Reference number: A24222; MUID:86030691
 A; Accession: A24222

A; Molecule type: protein
 A; Residues: 1-32 <SC3>
 R; Pradayrol, L.; Jornvall, H.; Mutt, V.; Ribet, A.
 FEBS Lett. 109; 55-58, 1980
 A; Title: N-terminally extended somatostatin: the primary structure of somatostatin-28.
 A; Reference number: A91273; MUID:80113258
 A; Accession: A91273
 A; Molecule type: protein
 A; Residues: 65-92 <PRA>
 A; Experimental source: intestine
 R; Schally, A.V.; Huang, W.Y.; Chang, R.C.C.; Arimura, A.; Redding, T.W.; Millar, R.P.;
 Proc. Natl. Acad. Sci. U.S.A. 77, 4489-4493, 1980
 A; Title: Isolation and structure of pro-somatostatin: a putative somatostatin precursor
 A; Reference number: A93854; MUID:81054799
 A; Accession: A93854
 A; Molecule type: protein
 A; Residues: 65-92 <SC2>
 A; Experimental source: hypothalamus
 R; Schally, A.V.; Dupont, A.; Arimura, A.; Redding, T.W.; Nishi, N.; Linthicum, G.L.; Sch
 Biochemistry 15, 509-514, 1976
 A; Title: Isolation and structure of somatostatin from porcine hypothalamus.
 A; Reference number: A90398; MUID:76136331
 A; Accession: A90398
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <BE2>
 C; Comment: Somatostatin inhibits the release of somatotropin.
 C; Superfamily: somatostatin
 C; Keywords: hormone; hypothalamus; intestine; neuropeptide
 F; 1-64/Domain: pro-somatostatin-28 #status experimental <PRO>
 F; 65-92/Product: somatostatin-14 #status experimental <M14>
 F; 79-92/Product: somatostatin-14 #status experimental <M14>
 F; 37/Binding site: carbohydrate (Asn) (covalent) #status absent
 F; 81-92/Disulfide bonds: #status absent

Query Match 22.8%; Score 136; DB 1; Length 92;
 Best Local Similarity 36.9%; Pred. No. 2.1e-07; Mismatches 15; Indels 26; Gaps 5;
 Matches 38; Conservative 38;
 Qy 24 AASOPDDDLASRRLQLRALAAALPHRGSGVSRWRWTFYPNCPCLRWRPRKVKGPKQLKAKE- 82
 1 APSDPRL---RQFLQKSLAAA---AGKQELAKYFLAE---LLSEPNOTENDALEPEDL 49
 Db 83 -----DLERSVDNLP---PRERKAGCKNFKNYKGFTSC 111
 50 SQAAEQDEMRLLEQRSANSNPAMAPRERKAGCKNFKNFWKTFtSC 92

RESULT 15

RIAFSI

Somatostatin I precursor - American goosefish
 N; Contains: somatostatin I
 C; Species: *Lophius americanus* (American goosefish)
 C; Date: 31-Mar-1981 #sequence revision 31-Mar-1981 #text_change 28-May-1999
 C; Accession: A93236; A93860; A91087; A01433
 R; Hobart, P.; Crawford, R.; Shen, L.; Pictet, R.; Rutter, W.J.
 Nature 288, 137-141, 1980
 A; Title: Cloning and sequence analysis of cDNAs encoding two distinct somatostatin-precu
 A; Reference number: A93236; MUID:81052423
 A; Accession: A93236

A; Molecule type: mRNA
 A; Residues: 1-121 <HOB>
 A; Cross-references: GB:V00640; GB:J00946; NID:g64028; PID:CAA23986.1; PID:g64029
 R; Goodman, R.H.; Jacobs, J.W.; Chin, W.W.; Lund, P.K.; Dee, P.C.; Habener, J.F.
 Proc. Natl. Acad. Sci. U.S.A. 77, 5869-5873, 1980

A; Title: Nucleotide sequence of a cloned structural gene coding for a precursor of p.
 A; Reference number: A93860; MUID:81077276
 A; Accession: A93860
 A; Molecule type: mRNA
 A; Residues: 2-20, 'V', 22-82, 'E', 84-121 <GOO>
 A; Experimental source: islet tissue (endocrine pancreas)
 R; Goodman, R.H.; Jacobs, J.W.; Chin, W.W.; Lund, P.K.; Dee, P.C.; Habener, J.F.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1682, 1982
 A; Contents: annotation; erratum
 R; Noe, B.D.; Spiess, J.; Rivier, J.E.; Vale, W.
 Endocrinology 105, 1410-1415, 1979
 A; Title: Isolation and characterization of somatostatin from anglerfish pancreatic l.
 A; Reference number: A91087; MUID:80046482
 A; Accession: A91087
 A; Molecule type: protein
 A; Residues: 108-121 <NOE>
 C; Superfamily: somatostatin
 C; Keywords: neuropeptide
 F; 1-24/Domain: signal sequence #status predicted <SIG>
 F; 108-121/Product: somatostatin I #status experimental <MAT>
 F; 110-121/Disulfide bonds: #status predicted
 A; Accession: A91087
 A; Molecule type: protein
 A; Residues: 65-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
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 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
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 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
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 A; Molecule type: protein
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 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
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 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
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 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
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 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
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 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
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 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
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 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
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 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
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 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
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 A; Accession: S13616
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 A; Residues: 79-92 <SC2>
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 A; Residues: 79-92 <SC2>
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 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
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 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
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 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
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 A; Residues: 79-92 <SC2>
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 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
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 A; Reference number: S13616; MUID:91160722
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 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
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 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnsen, A.H.; Holst, J.J.
 FEBS Lett. 27

RESULT 2

Q90Y43 PRELIMINARY; PRT; 115 AA.

AC Q90Y43; ID Q90Y43; PRELIMINARY; PRT; 115 AA.

DT 01-DEC-2001 (TREMBLrel: 19, Created)

DT 01-DEC-2001 (TREMBLrel: 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel: 19, Last annotation update)

DE PREPROSOMATOSTATIN.

OS Osteoglossum bicirrhosum (silver arawana).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha; Osteoglossiformes; Osteoglossidae; Osteoglossum.

OX NCBI_TAXID=109271;

RN [1]

RP SEQUENCE FROM N.A. Al-Mahrouki A.A.; Irwin D.M.; Youson J.H.;

RA "Characterization of variant somatostatin cDNAs from several osteoglossomorphs: molecular identification and comparative analysis.";

RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF292650; AAK97067.1; SEQUENCE 115 AA; 12791 MW; D65FBD7C6F1E4E4D CRC64;

SQ [1]

Query Match 39.5%; Score 236; DB 13; Length 115; Best Local Similarity 47.5%; Pred. No. 9.3e-19; Matches 58; Conservative 10; Mismatches 36; Indels 18; Gaps 4;

QY 1 MRVSOIHCALALLGLALAICSGQAAASQPDLDLQASRRLQLQRALAAALPHRSGVSEWRRTFY 60

DB 1 MKICQIHCALTLVLLGLVGLYCPASAQP--DIRYRSFLQRAHAAAMS----PQDWSKQA 53

QY 61 PNCPCLRRWPRKVKGPQ-----LKAKEDELDERSYD--NLPPRERKAGCKKNFVWKGFT 109

DB 54 VEELLSRLAPAQGEVPPQGAVSAADEEEEDVRYDERSLELLNNLPPRERKAGCKKNFVWKGFT 113

QY 110 SC 111

DB 114 SC 115

RESULT 3

Q90Y42 PRELIMINARY; PRT; 114 AA.

AC Q90Y42; ID Q90Y42; PRELIMINARY; PRT; 114 AA.

DT 01-DEC-2001 (TREMBLrel: 19, Created)

DT 01-DEC-2001 (TREMBLrel: 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel: 19, Last annotation update)

DE PREPROSOMATOSTATIN.

OS Pantodon buchholzii (Butterflyfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Pantodon.

OC Osteoglossiformes; Pantodontidae; Pantodon.

OX NCBI_TAXID=82276;

RN [1]

RP SEQUENCE FROM N.A. Al-Mahrouki A.A.; Irwin D.M.; Youson J.H.;

RA "Characterization of variant somatostatin cDNAs from several osteoglossomorphs: molecular identification and comparative analysis.";

RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF292651; AAK97068.1; SEQUENCE 114 AA; 12352 MW; 7E3D44CB6A27B12F CRC64;

SQ [1]

Query Match 38.3%; Score 228.5; DB 13; Length 114; Best Local Similarity 41.4%; Pred. No. 6.3e-18; Matches 55; Conservative 14; Mismatches 23; Indels 41; Gaps 5;

QY 1 MRVSOIHCALALLGLALAICSGQAAASQPDLDLQASRRLQLQRALAAALPHRSGVSEWRRTFY 60

DB 1 MKICQIHCALALLGLALAICSGQAAASQPDLDLQASRRLQLQRALAAALPHRSGVSEWRRTFY 60

Query Match 29.9%; Score 178.5; DB 13; Length 114;
 Best Local Similarity 40.8%; Pred. No. 2.4e-12;
 Matches 51; Conservative 13; Mismatches 36; Indels 25; Gaps 5;

Qy 1 MRVSQIHCALALLGLALAICSGQAAASOPDLDLASRRLQLRALAAALPHRSGVSEWRRTFY 60
 Db 1 MLIISTRQCALALLSIALPVSVAAPS---DLKRQLLQRSTIAP----ASKQELARY 51

Qy 61 PNCPCLWRPRKVKGPQLAKEDLERSVDN-----LPRERKAGCKNFYWK 106
 Db 52 TLAELLS-ELAQVEENALESDDLRGADQEEVRLELERAAGPPLA PRERKAGCKNFYWK 109

Qy 107 GFTSC 111
 Db 110 GFTSC 114

RESULT 6
 ID Q90XE1 PRELIMINARY; PRT; 116 AA.
 AC Q90XE1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SOMATOSTATIN
 OS Acipenser transmontanus (White sturgeon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
 OC Acipenserinae; Acipenser.
 OX NCBI_TAXID=7904;
 RN [1]
 SEQUENCE FROM N.A.
 TISSUE-BRAIN;
 RA Trabucchi M., Tostivint H., Lihrmann I., Sollars C., Vallarino M.,
 RA Dores R.M., Vaudry H.;
 RA "Polygenic expression of somatostatin in the sturgeon Acipenser
 transmontanus: molecular cloning and distribution of the mRNAs
 encoding two somatostatin precursors.";
 RT J. Comp. Neurol. 0:0-0(2001).
 RL EMBL; AF395849; AAL13248.1;
 DR 116 AA; 12616 MW; 72E0C3FF6C80650F CRC64;
 SQ SEQUENCE

Query Match 29.2%; Score 174.5; DB 13; Length 116;
 Best Local Similarity 38.1%; Pred. No. 6.8e-12;
 Matches 51; Conservative 15; Mismatches 27; Indels 41; Gaps 6;

Qy 1 MRVSQIHCALALLGLALAICSGQAA-SQPDDLDLASRRLQLRALAAALPHRSGVSEWRRTF 59
 Db 1 MLSSRLQCALAFLSALAVSSVAAAPSIDPRL---RQLQRTLAA---AGKQE---- 47

Qy 60 YPNCPCLWRPRKVKGPQLAKED-----LERSVDNLP---PRERK 97
 Db 48 -----LLKYSIAELLSLAQSENDALASDELSRAAEQNDVRLELERSANGNPAMAPRERK 102

Qy 98 AGCKNFYWKGFTSC 111
 Db 103 AGCKNFYWKGFTSC 116

RESULT 7
 ID Q9PRN9 PRELIMINARY; PRT; 28 AA.
 AC Q9PRN9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE GSS-28-SOMATOSTATIN-LIKE PEPTIDE.

Query Match 20.6%; Score 123; DB 13; Length 28;
 Best Local Similarity 84.0%; Pred. No. 7.9e-07;
 Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 87 SVDNLPPRERKAGCKNFYWKGFTSC 111
 Db 4 SSNHLPARERKAGCKNFYWKGFTSC 28

RESULT 8
 ID Q9PRV0 PRELIMINARY; PRT; 25 AA.
 AC Q9PRV0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SOMATOSTATIN-RELATED PEPTIDE.
 OS Anguilla japonica (Japanese eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguilloidei;
 OC Anguillidae; Anguilla.
 OX NCBI_TAXID=7937;

Query Match 19.1%; Score 114; DB 13; Length 25;
 Best Local Similarity 84.0%; Pred. No. 7e-06;
 Matches 21; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 87 SVDNLPPRERKAGCKNFYWKGFTSC 111
 Db 1 SVDNQQGRERKAGCKNFYWKGFTSC 25

RESULT 9
 ID Q9DDE4 PRELIMINARY; PRT; 107 AA.
 AC Q9DDE4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SOMATOSTATIN.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Danio.
 OX NCBI_TAXID=7955;

Query Match 12.7%; Score 76; DB 16; Length 251;
 Best Local Similarity 33.3%; Pred. No. 1.5;
 Matches 29; Conservative 15; Mismatches 23; Indels 20; Gaps 5;

Q9PZX3 PRELIMINARY; PRT; 1242 AA.
 AC Q9PZX3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE STRUCTURAL POLYPROTEIN.
 OS Eastern equine encephalitis virus (Eastern equine encephalomyelitis virus).
 OC ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 NCBI_TAXID=11021;
 [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=FL93-939;
 RA Brault A.C., Powers A.M., Kang W., Tesh R.B., Shope R.E., Weaver S.C.,
 "Genetic and Antigenic Diversity among Eastern Equine Encephalitis
 Viruses from North, Central and South America.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AFI15954; AAF04796.1;
 DR HSSP; P03315; 1VCP;
 DR InterPro; IPR001836; Alpha_core;
 DR InterPro; IPR002548; Alpha_E1_glycop;
 DR InterPro; IPR002533; Alpha_E3_glycop;
 DR InterPro; IPR000930; Togavirin.
 DR Pfam; PF00944; Alpha_core; 1;
 DR Pfam; PF01589; Alpha_E1_glycop; 1;
 DR Pfam; PF00943; Alpha_E2_glycop; 1;
 DR Pfam; PF01563; Alpha_E3_glycop; 1;
 DR PRINTS; PR00798; TOGAVIRIN.
 KW Polyprotein.
 SQ SEQUENCE 1242 AA; 1137613 MW; 6E474EB2A91FF4CD CRC64;

Query Match 12.9%; Score 77; DB 12; Length 1242;
 Best Local Similarity 44.0%; Pred. No. 6.8;
 Matches 22; Conservative 3; Mismatches 9; Indels 16; Gaps 3;

Q9HG9 PRELIMINARY; PRT; 251 AA.
 AC Q9HG9;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE MLL2874 PROTEIN.
 GN MLL2874.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 NCBI_TAXID=381;
 [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 MEDLINE=21082930; PubMed=11214968;
 RX Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsuno A., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpou S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338 (2000).
 DR AP003000; BAB49897.1;
 KW Complete proteome.
 SQ SEQUENCE 251 AA; 27987 MW; 45709CC6A71EDD2AA CRC64;

Query Match 12.6%; Score 75.5%; DB 12; Length 259;
 Best Local Similarity 38.5%; Pred. No. 1.8;
 Matches 20; Conservative 7; Mismatches 8; Indels 17; Gaps 3;

Q98HG9 PRELIMINARY; PRT; 251 AA.
 AC Q98HG9;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE MLL2874 PROTEIN.
 GN MLL2874.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 NCBI_TAXID=381;
 [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 MEDLINE=21082930; PubMed=11214968;
 RX Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsuno A., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpou S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338 (2000).
 DR AP003000; BAB49897.1;
 KW Complete proteome.
 SQ SEQUENCE 251 AA; 27987 MW; 45709CC6A71EDD2AA CRC64;

Search completed: June 13, 2002, 12:31:02
 Job time: 484 sec

PT Peptide 98..111
 PT /note: "SS-14 variant peptide"
 XX CA2325169-A1.
 XX 03-JUN-2001.
 PD 01-DEC-2000; 2000CA-2325169.
 XX PR 03-DEC-1999; 99US-0168934.
 XX PA (NDSU-) NDSU RES FOUND.
 XX PI Sheridan MA, Moore CA, Kittelson JD;
 XX DR WPI: 2001-425997/46.
 DR N-PSDB; AAS12935.
 XX New somatostatin polypeptides derived from Oncorhynchus mykiss, useful
 for treating diabetes mellitus, acromegaly, gastrinoma, acquired
 immunodeficiency syndrome and neurological disorders

PS Claim 1; Fig 3; 52pp; English.
 XX The invention relates to an Oncorhynchus mykiss somatostatin polypeptide
 containing a portion of preprosomatostatin I (PPSS-I) and/or a portion of
 preprosomatostatin II (PPSS-II). The protein sequences and their
 associated polynucleotides are useful for identifying modified
 somatostatin polypeptides which functions as a somatostatin agonist useful
 for research, therapeutics or diagnostics, including medical and
 veterinary applications. The wild-type somatostatin and its modified
 version are useful for treating hypersecretion from endocrine tumours in
 the pituitary (e.g. acromegaly) or gastrointestinal tissues (e.g.
 gastrinoma, glucagonoma, carcinoid syndrome), to cause tumour shrinkage
 through their effects on cell proliferation and apoptosis and as adjuncts
 in the treatment of diabetes mellitus via inhibition of growth hormone
 and glucagon. In addition, dysfunctional somatostatin secretion is
 associated with disorders (e.g. AIDS) and various
 neurological disorders (e.g. epilepsy, Alzheimer's disease and
 Huntington's disease) and somatostatin antagonists are effective in the
 treatment of such conditions. Nucleic acids encoding the polypeptides are
 useful in gene therapy and fusion peptides can be targeted to neoplasms
 and their metastases, inhibiting the release of their secretory products.
 This sequence represents O. Mykiss PPSS-II', protein.
 Note: The features for this sequence are specifically claimed in the
 specification.

XX Sequence 111 AA;

Query Match 100.0%; Score 597; DB 22; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.6e-63;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVSQIHCALALLGLALAICSOGAASQPDPDLDLASRRLQLQRALAAALPHRSGVSEWRWRTFY 60
 DB 1 mrvsqihcalallglalaicsogaasqpdpdldlasrrlqlqralaaalphrsgvsewrwrtfy 60
 QY 61 PNCPCLWRPRPKVGPQLKAKEDLERSVVDNPPRERKAGCKNFKYWKGFTSC 111
 DB 61 pncpclwrprpkvgpqlkakedlersvvdnpprerkagcknfywkgtsc 111

RESULT 2
 AAU07667 ID AAU07667 standard; Protein; 115 AA.
 XX AC AAU07667;
 XX DT 04-DEC-2001 (first entry)
 XX DE Rainbow trout preprosomatostatin II (PPSS-II') polypeptide.
 XX

XX The invention relates to an Oncorhynchus mykiss somatostatin polypeptide
 containing a portion of preprosomatostatin I (PPSS-I) and/or a portion of
 preprosomatostatin II (PPSS-II). The protein sequences and their
 associated polynucleotides are useful for identifying modified
 somatostatin polypeptides which functions as a somatostatin agonist useful
 for research, therapeutics or diagnostics, including medical and
 veterinary applications. The wild-type somatostatin and its modified
 version are useful for treating hypersecretion from endocrine tumours in
 the pituitary (e.g. acromegaly) or gastrointestinal tissues (e.g.
 gastrinoma, glucagonoma, carcinoid syndrome), to cause tumour shrinkage
 through their effects on cell proliferation and apoptosis and as adjuncts
 in the treatment of diabetes mellitus via inhibition of growth hormone
 and glucagon. In addition, dysfunctional somatostatin secretion is
 associated with acquired immunodeficiency syndrome (AIDS) and various
 neurological disorders (e.g. epilepsy, Alzheimer's disease and
 Huntington's disease) and somatostatin antagonists are effective in the
 treatment of such conditions. Nucleic acids encoding the polypeptides are
 useful in gene therapy and fusion peptides can be targeted to neoplasms
 and their metastases, inhibiting the release of their secretory products.
 This sequence represents O. Mykiss PPSS-II', protein.
 Note: The features for this sequence are specifically claimed in the
 specification.

XX

QY	1	MRVSQIHCALALLGALAIICSGAASQDLDLASRLLQRALAAALPHRSGVSEWRWTFY	60	Score 40.7%; DB 22; Length 115;	56 W-----RTFYPCPCLRWPRKVKGPQLKAKEDLERSVD--NLPRPR 96	
Best Local Similarity	83.9%	Pred. No. 9.3e-50;	3;	Mismatches	59 wskraveellaqmslpeatfq-----reaedassmategrmlersvdstnnlppr 110	
Matches	99;	Conservative	3;	Indels	10;	Gaps 4;
Db	1	mkvcrhcalallgalaicsgqaasqpdldrsrrlgraraalphrsgvsewrwtfy	60			
QY	61	PNCPCPCLRWPRKVKGPQLKAKED---LERSV---DNLPPRERKAGCKNFTYWKGFTSC	111		97 KAGCKKNFTYWKGFTSC 111	
Db	61	pncpcl--rprkvkcp-agakedlrvelersvgnpnnlpprerkagcknfywkqftsc	115		111 kagcknfywkqftsc 125	
RESULT	3					
	AAP20029	ID AAP20029 standard; Protein; 125 AA.				
XX	DE	Sequence of preprosomatostatin-2 encoded on pLas2.				
XX	KW	Somatostatin; growth hormone; peptide hormone; secretion.				
XX	FH	Key				
FT	Protein	112..125				
FT	label=	Somatostatin II				
XX	PN	EP46669-A.				
XX	PD	03-MAR-1982.				
XX	PF	21-AUG-1981;	81EP-0303825.			
XX	PR	25-AUG-1980;	80US-0181046.			
XX	PA	(REGC) UNIV OF CALIFORNIA.				
XX	PI	Hobart P, Crawford R, Pictet RL, Rutter WJ;				
XX	DR	WPI; 1982-18113E/10.				
DR	N-PSDB; AAN20034.					
XX	PPT	New somatostatin and precursors - produced by transformed				
	microorganisms					
FS	Example; Fig 3; 50pp; English.					
XX	The inventors claim preprosomatostatin-1, prosomatostatin-1, preprosomatostatin-2, prosomatostatin-2 and somatostatin-2; and DNA encoding them. The translation of somatostatin mRNA yields a precursor (prepro S1) containing a signal peptide which may be released during the transit into the endoplasmic reticulum, and the resultant precursor (pro S1) is subsequently cleaved to yield S1 itself. The prepeptide portion of prepro S1 is probably about 20-25 bases long. Translation of pLas2 predicts the sequence of a 125 AA peptide which surprisingly contains a 14 AA sequence at its carboxy terminus which differs from S1 by only 2 AAs, and is termed somatostatin 2 (S2).					
XX	SQ	Sequence 125 AA;				
XX	SQ	Score 194; DB 3; Length 125;	29.6%; Score 176.5; DB 21; Length 116;			
QY	5	QIHCALALLGLALAI-CSQGAASQPDLDLASRLLQRALAAALPHRSGVSEWRWTFYPCNC	63	Best Local Similarity 38.2%; Pred. No. 3.2e-13;	5	
Matches	47;	Conservative 19;	Mismatches 30;	Indels 27; Gaps 6		
Db	5	rlqcalalaalsivialgcvtgapsdpri---rqflqkslaaa---agkqelakyflae-	55			
QY	6	IHCALALLGLALICSGAASQ-----PDLDLASSRRLQRALAAALPHRSGVSE	55	64. PCLRWPRKVKGPQLKAKE-----DLERSVDNL-----PRERKAGCKKNFTWKG	108	

Db 56 -llsepqntdalepedlsqaaeqdemrlelqrsansmpamprerkagcknfwktf 113
 QY 109 TSC 111
 Db 114 tsc 116

RESULT 5
 AAU07666 standard; Protein; 114 AA.
 XX
 AAU07666;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 Rainbow trout preprosomatostatin I (PPSS-I) polypeptide.
 DE
 XX
 Rainbow trout; somatostatin; preprosomatostatin; hypersecretion; PPSS-I;
 PPSS-II'; PPSS-III'; endocrine tumour; pituitary gland; glucagonoma; AIDS;
 gastronenteropancreatic tissue; acromegaly; gastrinoma; diabetes mellitus;
 carcinoid syndrome; cell proliferation; apoptosis; growth hormone;
 glucagon; acquired immunodeficiency syndrome; neurological disorder; HIV;
 epilepsy; Alzheimer's disease; Huntington's disease; neuroprotective;
 neoplasm; metastasis; gene therapy; antidiabetic; nootropic; cytostatic;
 anti-human immunodeficiency virus; osteopathic; anticonvulsant.
 XX
 OS Oncorhynchus mykiss.
 XX
 Key Location/Qualifiers
 Peptide 1..24
 FT /note- "Signal peptide"
 Protein 1..88
 FT /note- "PPSS-I pro-sequence"
 Protein 25..114
 FT /note- "Mature PPSS-II"
 Peptide 89..100
 FT /note- "Prosomatostatin I"
 FT 99..100
 Cleavage-site /note- "Dibasic cleavage site"
 Peptide 101..114
 FT /note- "SS-14 peptide"
 XX
 CA2325169-A1.
 PN 03-JUN-2001.
 XX
 01-DEC-2000; 2000CA-2325169.
 PF 03-DEC-1999; 99US-0168934.
 PR (NDSU-) NDSU RES FOUND.
 XX
 PA Sheridan MA, Moore CA, Kittelson JD;
 XX
 WPI; 2001-425997/46.
 DR N-PSDB; AAS12933.
 XX
 New somatostatin polypeptides derived from Oncorhynchus mykiss, useful
 for treating diabetes mellitus, acromegaly, gastrinoma, acquired
 immunodeficiency syndrome and neurological disorders -
 XX
 Claim 1; Fig 2; 52pp; English.
 PS
 XX
 The invention relates to an Oncorhynchus mykiss somatostatin polypeptide
 containing a portion of preprosomatostatin I (PPSS-I) and/or a portion of
 preprosomatostatin II (PPSS-II). The protein sequences and their
 associated polynucleotides are useful for identifying modified
 somatostatin polypeptides which functions as a somatostatin agonist useful
 for research, therapeutics or diagnostics, including medical and
 veterinary applications. The wild-type somatostatin and its modified
 version are useful for treating hypersecretion from endocrine tumours in
 the pituitary (e.g. acromegaly) or gastronenteropancreatic tissues (e.g.
 gastrinoma, glucagonoma, carcinoid syndrome), to cause tumour shrinkage
 through their effects on cell proliferation and apoptosis and as adjuncts
 in the treatment of diabetes mellitus via inhibition of growth hormone
 and glucagon. In addition, dysfunctional somatostatin secretion is
 associated with acquired immunodeficiency syndrome (AIDS) and various
 neurological disorders (e.g. epilepsy, Alzheimer's disease and
 Huntington's disease) and somatostatin antagonists are effective in the
 treatment of such conditions. Nucleic acids encoding the polypeptides are
 useful in gene therapy and fusion peptides can be targeted to neoplasms
 and their metastases, inhibiting the release of their secretory products.
 XX
 Note: The features for this sequence are specifically claimed in the
 specification.
 XX
 Sequence 114 AA;

Query Match 27.6%; Score 164.5; DB 22; Length 114;
 Best Local Similarity 38.7%; Pred. No. 8.5e-12;
 Matches 48; Conservative 15; Mismatches 38; Indels 23; Gaps 5;

Qy 1 MRVSQIHCNALLGLALACSQGAAASQPDLLASRRLQLQRLANALPHRSGVSERWRTFY 60
 Db 1 mlstrvqcalislaissvaaps---daklrqlqrslmap---agkqgelarntl 53

Qy 61 PNCPCCLRWRPRKVKGQPLK-----AKEDLERSVDNLPL-----PRERKAGCKNFXWKG 107
 Db 54 ve---llselahveneaielddmshgveqedvdlelerapgvlaprerkagcknffwkt 110

Qy 108 FTSC 111
 Db 111 ftsc 114

RESULT 6
 AAP61714 standard; Protein; 28 AA.
 ID AAP61714
 XX AAP61714
 AC AAP61714;
 XX DT 28-JUL-1991 (first entry)
 DE Somatostatin-28 analogue.
 XX RW Somatostatin-28; insulin-selective; insulinoma.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 23
 FT /label= Hyl, Lys
 XX EP173527-A.
 XX PN
 XX PD 05-MAR-1986.
 XX PF 16-AUG-1985; 85EP-0305867.
 XX PR 31-AUG-1984; 84US-0646610.
 XX PA (SALK) SALK INST FOR BIOL STUD.
 XX PI Spless J, Noe BD;
 XX DR WPI; 1986-063363/10.
 XX PT Angler fish somatostatin-28 and analogue and fragment - useful in
 PT inhibiting insulin secretion in insulinoma.
 XX PS Claim 4; Page 18; 19pp; English.

The protein sequence is an insulin-selective analogue of anglerfish somatostatin-28, which is more potent than somatostatin-14 or somatostatin-28 in inhibiting insulin secretion for treatment of insulinoma.

Sequence 28 AA;

Query Match 22.1%; Score 132; DB 7; Length 28;
Best Local Similarity 88.0%; Pred. No. 1.2e-08;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 87 SVDNLPPRERKAGCKNFKYWKGGFTSC 111
Db 4 stnnlpprerkagcknfywxgftsc 28

RESULT 7

ID AAP90989 standard; peptide; 28 AA.

X C AAP90989;

XX DT 08-JUN-1990 (first entry)

XX DE Analogue of anglerfish somatostatin 28.

XX KW Somatostatin 28; SS-28; analogue; insulin secretion inhibitor; insulinoma; gastric acid secretion; thermoregulation. Anglerfish.

XX OS US4816438-A.

XX FH Key Location/Qualifiers

FT Disulfide-bond 17 /note="Bonded to Cys-28"

FT Disulfide-bond 28 /note="Bonded to Cys-17"

FT Misc-difference 23 /label=Lys, Hyl

FT Region 15..28 /note="Also claimed"

XX PN 87US-0033295.

XX PD 28-MAR-1989.

XX PF 01-APR-1987; 87US-0033295.

XX CR 01-APR-1987; 87US-0033295.

XX R 31-AUG-1984; 84US-0646610.

XX PA (SALK) SALK INST FOR BIOL STUD.

XX SPIESS J, Noe BD;

XX WPI; 1989-113910/15.

XX PT Angler fish somatostatin-28 and fragments - useful in inhibiting insulin secretion and insulinoma

XX PS Claim 1; page 65; 8PP; English.

CC It is called ASS-28 because it is an analogue of anglerfish somatostatin (SS-28). It is more potent than either somatostatin 14 (SS-14) or SS-28 at inhibiting insulin secretion for the treatment of insulinoma. The 14-residue C-terminal peptide is also claimed (ASS-14). ASS-14 is useful for inhibiting insulin secretion by the pancreas. ASS-28 and ASS-28 may be useful for decreasing gastric acid secretion and influencing thermoregulation. Their reduced linear forms, wherein the disulphide bridge is not present and is replaced by H, is also claimed.

XX SQ Sequence 28 AA;

Query Match 22.1%; Score 132; DB 10; Length 28;
Best Local Similarity 88.0%; Pred. No. 1.2e-08;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 87 SVDNLPPRERKAGCKNFKYWKGGFTSC 111

Db 4 stnnlpprerkagcknfywxgftsc 28

RESULT 8

ID AAP20028 standard; Protein; 121 AA.

XX AC AAP20028;

XX DT 14-AUG-1992 (first entry)

XX DE Sequence of preprosomatostatin-1 encoded on pLAs1.

XX KW Somatostatin; growth hormone; peptide hormone; secretion.

XX KEY Location/Qualifiers

FT Protein 108..121

FT /label= Somatostatin I

XX EP46669-A.

XX PD 03-MAR-1982.

XX PF 21-AUG-1981; 81EP-0303825.

XX PR 25-AUG-1980; 80US-0181046.

XX PA (REGC) UNIV OF CALIFORNIA.

XX PI Hobart P, Crawford R, Pictet RL, Rutter WJ,

XX WPI; 1982-18113E/10.

XX DR N-PSDB; AAN20033.

XX PT New somatostatin and precursors - produced by transformed microorganisms

XX Example; Fig 3; 50PP; English.

CC The inventors claim preprosomatostatin-1, prosomatostatin-1, preprosomatostatin-2, prosomatostatin-2 and somatostatin-2; and DNA encoding them. The translation of somatostatin mRNA yields a precursor (prepro S1) containing a signal peptide which may be released during the translaton into the endoplasmic reticulum, and the resulting precursor (pro S1) is subsequently cleaved to yield S1 itself. The prepeptide portion of prepro S1 is probably about 20-25 bases long. Translation of pLAs1 predicts the sequence of a 125 AA peptide which surprisingly contains a 14 AA sequence at its carboxy terminus which differs from S1 by only 2 AAs, and is termed somatostatin 2 (S2).

XX SQ Sequence 121 AA;

Query Match 22.0%; Score 131.5; DB 3; Length 121;
Best Local Similarity 37.9%; Pred. No. 8.1e-08;
Matches 47; Conservative 5; Mismatches 47; Indels 25; Gaps 5;

Qy 4 SQIHCALALLGLALAICSGQAAASQDLDLASSRRLQQR-----ALAAALPHRS 50

Db 7 srirclivllisitasiscsfagqrdskl--rliihryplqgskqdmttrsailaellsdl 64

Qy 51 GVSERWRTFYPNCPLRWRPRVKGPQLKAKEDLERSVDN---LPPRERKAGCKNFKYWKG 107

Db 65 lgenealeenplae----ggpe-dahadleraasggpliaprerkagcknfwkt 117

XX WO20069900-A2.
 PN XX 10-OCT-1996; 96IL-0119403.
 PD XX 12-SEP-1996; 96IL-0119250.
 XX PA (COHEN/) COHEN Y.
 XX PI Cohen Y;
 XX DR WPI; 1998-271636/24.
 XX PT Composition for treatment of the risk factors of syndrome X of Reaven - (hyperinsulinaemia syndrome) comprises somatostatin, diazoxide, cyclothiazide (or their analogues) and/or metformin
 PA (CONJ-) CONJUCHEM INC.
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX DR WPI; 2001-112059/12.
 XX PT Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
 PT PT
 XX S Disclosure; Page 252; 733pp; English.
 XX The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
 XX SQ Sequence 25 AA;

Query Match 17.6%; Score 105; DB 19; Length 28;
 Best Local Similarity 81.0%; Pred. No. 2e-05;
 Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 OS db 91 LPPRERKAGCKNFWKGFTSC 111
 : ||||| :||| :||| :|||
 5 maprerkagcknfwkftftsc 25

RESULT 12
 AAW51859 10-SEP-1998 (first entry)
 ID AAW51859 standard; peptide; 28 AA.
 XX DE Somatostatin analogue for the treatment of syndrome X of Reaven.
 XX KW Somatostatin analogue; syndrome X of Reaven; hyperinsulinaemia syndrome;
 KW diazoxide; cyclothiazide; metformin.
 OS Synthetic.
 XX PN WO9810786-A2.
 XX PD 19-MAR-1998.
 XX PF 10-SEP-1997; 97WO-IL00301.

XX PR 10-OCT-1996; 96IL-0119403.
 PR 12-SEP-1996; 96IL-0119250.
 XX PA (COHEN/) COHEN Y.
 XX PI Cohen Y;
 XX DR WPI; 1998-271636/24.
 XX PT Composition for treatment of the risk factors of syndrome X of Reaven - (hyperinsulinaemia syndrome) comprises somatostatin, diazoxide, cyclothiazide (or their analogues) and/or metformin
 XX PS Claim 42; Page 41; 45pp; English.
 XX The invention relates to a pharmaceutical composition for treatment of the risk factors of syndrome X of Reaven (hyperinsulinaemia syndrome). It comprises somatostatin, diazoxide, cyclothiazide (or an analogue of one of these) or metformin as the active ingredient. The composition reduces resistance to insulin, and so treats and prevents all the associated risk factors at once. The risk factors are hypertension, dyslipidaemia (raised triglyceride and LDL levels with reduced HDL levels), shorter coagulation time due to increased Plasminogen Activator Inhibitor-1 levels, core obesity, glucose intolerance hyperinsulinaemia. The composition reduces the incidence of ischaemic heart disease, cerebrovascular disorders, intermittent claudication, ischaemic bowel disease, impotence due to peripheral vascular disease, hypercoagulation (e.g. renal vein thrombosis), obesity and glucose intolerance. The present sequence represents a specifically claimed somatostatin analogue
 XX SQ Sequence 28 AA;

Query Match 17.6%; Score 105; DB 19; Length 28;
 Best Local Similarity 81.0%; Pred. No. 2e-05;
 Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 OS db 91 LPPRERKAGCKNFWKGFTSC 111
 : ||||| :||| :||| :|||
 8 maprerkagcknfwkftftsc 28

RESULT 13
 AAY28703 07-OCT-1999 (first entry)
 ID AAY28703 standard; peptide; 28 AA.
 XX AC AAY28703;
 XX DE DE
 XX KW Mouse somatostatin SS-28 hormone.
 KW thyroid stimulating hormone; octreotide; cell-based delivery of insulin;
 KW glucose-stimulated insulin secretion; SSTRV; somatostatin receptor
 mouse somatostatin receptor type V gene; diabetes
 XX OS Mus musculus.
 XX PN WO935242-A1.
 XX PD 15-JUL-1999.
 XX PR 11-JAN-1999; 99WO-US00633.
 XX PR 03-JUN-1998; 98US-0087848.
 PR 12-JAN-1998; 98US-0071193.
 PR 12-JAN-1998; 98US-0071209.
 PR 12-JAN-1998; 98US-0072556.
 PR 03-JUN-1998; 98US-0087821.
 XX PA (BETA-) BETAGENE INC.

XX PI Clark SA, Quaade C;
 XX WPI; 1999-444195/37.
 XX New defined medium for culture of neuroendocrine cells, e.g. of
 PT insulin-secreting cells
 XX Example 8; Page 143; 312PP; English.
 PS The present sequence is a mouse somatostatin (SS-28) hormone which
 CC was found to inhibit the release of growth hormone, thyroid stimulating
 CC hormone, insulin and glucagon. In addition, SS-28 and its analogue
 CC Octreotide may inhibit growth of some tumours. The hormone was
 CC used to study its effect on glucose-stimulated insulin secretion in
 CC high expressing and non-expressing clones of mouse somatostatin
 CC receptor, type V gene (SSTRV). The insulin secretion was highly inhibited
 CC in the high expressing clone as compared to the non-expressing clone
 CC because the high expressing clone showed high sensitivity to
 CC somatostatin. The hormone effectively inhibits insulin secretion in the
 CC absence of glucose. The somatostatin receptor can be introduced in cell
 CC lines, used in cell-based delivery of insulin for treating diabetes, for
 CC precise regulation of insulin release.
 XX Sequence 28 AA;
 SQ Query Match 17.6%; Score 105; DB 20; Length 28;
 Best Local Similarity 81.0%; Pred. No. 2e-05;
 Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 RESULT 15
 Qy 91 LPPRERKAGCKKNFKWKGFTSC 111
 Db 8 maprerkagcknffwktftsc 28
 YY AAY242384 standard; peptide: 28 AA.
 YY AAY242384;
 DT 20-SEP-1999 (first entry)
 DE Somatostatin peptide hormone SS-28.
 XX Glucagon-like Peptide I receptor; GLP-1 receptor; drug screening;
 KW secretory function; immortalised neuroendocrine secretory cell;
 KW regulation; diabetes; insulin secretion; neuroendocrine-based disorder;
 KW Parkinson's disease; athyrotic cretinism; Addison's disease.
 OS Mus musculus.
 XX WO9935495-A2.
 XX 15-JUL-1999.
 PD 11-JAN-1999; 99WO-US00631.
 XX (BETA-) BETAGENE INC.
 PA 03-JUN-1998; 98US-0087848.
 PR 12-JAN-1998; 98US-0071193.
 PR 12-JAN-1998; 98US-0071209.
 PR 12-JAN-1998; 98US-0072556.
 PR 03-JUN-1998; 98US-0087821.
 XX (BETA-) BETAGENE INC.
 PA Clark SA, Quaade C, Thigpen AE;
 XX WPI; 1999-430454/36.
 XX New modulators of secretory function, used to control peptide
 PT secretion from cells in vivo or in vitro, specifically for treating
 PR diabetes

PT diabetes
 XX Example 8; Page 153-154; 309PP; English.
 PS The present invention describes a method for identifying modulators (I) of secretory function by treating an immortalised cell, having a stable secretion caused by the compound, with a test compound and detecting any change in polypeptides from cells, in vivo or in vitro. Specifically they are used but can also be used in cases of other neuroendocrine-based disorders such as Parkinson's disease, athyrotic cretinism and Addison's disease. The method uses engineered, immortalised cells that are available in large amounts, with a stable and predictable phenotype. They allow screening to be performed in vivo. The present sequence represents a somatostatin peptide hormone SS-28 used in an example from the present invention.
 XX Sequence 28 AA;
 SQ Query Match 17.6%; Score 105; DB 20; Length 28;
 Best Local Similarity 81.0%; Pred. No. 2e-05;
 Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 YY Qy 91 LPPRERKAGCKKNFKWKGFTSC 111
 Db 8 maprerkagcknffwktftsc 28
 YY AAY242384 standard; peptide: 28 AA.
 YY AAY242384;
 DT 15-SEP-1999 (first entry)
 DE Peptide hormone somatostatin SS-28.
 XX AAY242384 standard; peptide: 28 AA.
 YY AAY242384;
 DT 15-SEP-1999 (first entry)
 DE Somatostatin peptide hormone SS-28.
 XX Glucagon-like Peptide I receptor; GLP-1 receptor; drug screening;
 KW secretory function; immortalised neuroendocrine secretory cell;
 KW regulation; diabetes; insulin secretion; neuroendocrine-based disorder;
 KW Parkinson's disease; athyrotic cretinism; Addison's disease.
 OS Mus musculus.
 XX WO9935495-A2.
 XX 15-JUL-1999.
 PD 11-JAN-1999; 99WO-US00631.
 XX (BETA-) BETAGENE INC.
 PA 03-JUN-1998; 98US-0087848.
 PR 12-JAN-1998; 98US-0071193.
 PR 12-JAN-1998; 98US-0071209.
 PR 12-JAN-1998; 98US-0072556.
 PR 03-JUN-1998; 98US-0087821.
 XX (BETA-) BETAGENE INC.
 PA Clark SA, Quaade C, Thigpen AE;
 XX WPI; 1999-430454/36.
 XX New modulators of secretory function, used to control peptide
 PT secretion from cells in vivo or in vitro, specifically for treating
 PR diabetes

PT diabetes

XX Example 8; Page 148; 318PP; English.

XX The present invention describes immortalized neuroendocrine cells (A) that stably secrete a polypeptide hormone (I) contain an expression region that includes a transgene (TG), linked to a promoter functional in eukaryotic cells, such that expression of TG increases sensitivity

cc of the cells to a modulator of (I) secretion. (A) are specifically
cc used, by transplantation, to treat diabetes or hypoglycaemia (especially
cc where associated with insulin therapy) but more generally are used to
cc express, *in vivo*, a wide range of therapeutic hormones, enzymes,
cc amidated proteins and growth factors. Also engineered neuroendocrine
cc cells are used to identify new therapeutic agents or drug targets.
(A) have a stable phenotype and particularly inducible glucagon
cc secretion and glucose counter-regulatory capacities, i.e. they balance
cc the hyperglycaemic effects of beta-cell loss and the hypoglycaemic
cc effects of administered insulin. Since they are of human origin, they
cc are less likely to suffer immune rejection than xenografts. The present
cc sequence represents the peptide hormone somatostatin SS-28 used in an
cc example from the present invention.

xx Sequence 28 AA;

Query Match 17.6%; Score 105; DB 20; Length 28;
Best Local Similarity 81.0%; Pred. No. 2e-05;
Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
91 LPPRERKAGCKNFKWKGFTSC 111
:|||||:||||:|||||
Db 8 maprerkagcknffwktftsc 28

Search completed: June 13, 2002, 12:22:21
Job time: 274 sec

Qy 67 RWRPRKVKGPKLAKKE-----DLERSVDNL-----PRERKAGCKNFYWKGFTSC 111
 Db 51 LSEPNOTEADLEPEDLPOAAEODEMLQLRSANSNPAMAPRERKAGCKNFYWKTFSC 110

RESULT 2
 US-08-648-322-2
 Sequence 2, Application US/08648322
 Patent No. 6074872
 GENERAL INFORMATION:
 APPLICANT: Sutcliffe, Gregor J.
 de Lecea, Luis
 TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,
 COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
 STREET: 10666 NO. 6074872th Torrey Pines Road, TPC-8
 CITY: La Jolla
 STATE: California
 COUNTRY: US
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/001472
 FILING DATE: Herewith
 CLASSIFICATION:
 APPLICATION NUMBER: US 60/033,980
 FILING DATE: 31-DEC-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/037,386
 FILING DATE: 07-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.0430002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-001472-3

NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: 519.0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-2937
 TELEFAX: (619) 554-6312
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-648-322-2

Query Match 14.6%; Score 87; DB 3; Length 112;

Best Local Similarity 25.2%; Pred. No. 0.0016;

Matches 30; Conservative 9; Mismatches 42; Indels 38; Gaps 4;

Qy 20 CSQGAASQPDLASRRLQLRALAAALPHRSGVSER-----WRTF 59
 Db 4 CSTRGKRPSPSLLLSSGIASALPESGPTGDSVQDATGRRTGLLTFLAWHH-- 61

Qy 60 YPNCPCLWRPRKVKKG-----POLKAKEDLERSVDNLPPRERKAGCKNFYWKFTSC 111
 Db 62 -----EVASQDSSSTAFEGGTPELSKRQ--ERPLQQPHRDKKKPCKKNFWKTFSSC 111

Query Match 14.6%; Score 87; DB 3; Length 112;
 Best Local Similarity 25.2%; Pred. No. 0.0016;
 Matches 30; Conservative 9; Mismatches 42; Indels 38; Gaps 4;
 Qy 20 CSQGAASQPDLASRRLQLRALAAALPHRSGVSER-----WRTF 59
 Db 4 CSTRGKRPSPSLLLSSGIASALPESGPTGDSVQDATGRRTGLLTFLAWHH-- 61

Qy 60 YPNCPCLWRPRKVKKG-----POLKAKEDLERSVDNLPPRERKAGCKNFYWKFTSC 111
 Db 62 -----EVASQDSSSTAFEGGTPELSKRQ--ERPLQQPHRDKKKPCKKNFWKTFSSC 111

RESULT 4
 US-08-648-322-6
 Sequence 6, Application US/08648322
 Patent No. 6074872
 GENERAL INFORMATION:
 APPLICANT: Sutcliffe, Gregor J.
 de Lecea, Luis
 TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,
 COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 STREET: 10666 No. 6074872th Torrey Pines Road, TPC-8
 CITY: La Jolla
 STATE: California
 COUNTRY: US
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/648,322
 FILING DATE:

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: 519.0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-2937
 TELEFAX: (619) 554-6312
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 85 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: C-terminal
 US-08-648-322-6

RESULT 5
 Sequence 2, Application US/09001472
 Patent No. 6232100

GENERAL INFORMATION:
 APPLICANT: OLSEN, HENRIK S.
 APPLICANT: RUBEN, STEVEN M.
 TITLE OF INVENTION: CORTISTATIN POLYPEPTIDES
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/001,472
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,980
 FILING DATE: 31-DEC-1996

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/037,386
 FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.04300002
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 105 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-001-472-2

Query Match 13.5%; Score 80.5; DB 4; Length 105;
 Best Local Similarity 27.7%; Pred. No. 0.0098;
 Matches 26; Conservative 12; Mismatches 37; Indels 19; Gaps 4;

Qy 37 LLQRALAAALPHRGVSEWRRTFYPNCPLR-----WRPRKVKGPOI-KAK 81
 Db 11 LLSGATATAALPLEGGPTGRDSEHMQEAAAGRKSLLTFLAWWFETWSQASAGPLIGEEA 70

Qy 82 EDLERSVDNLPP----RERKAGCKKNFYWKGFTSC 111
 Db 71 REVARRQEAPPQOSARRDRMPCRNFFWKTTPSSC 104

RESULT 6
 Sequence 5, Application US/08648322
 Patent No. 6074872

GENERAL INFORMATION:
 APPLICANT: Sutcliffe, Gregor J.
 APPLICANT: de Lecea, Luis
 TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,
 TITLE OF INVENTION: COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
 STREET: 10666 No. 6074872nd Torrey Pines Road, TPC-8
 CITY: La Jolla
 STATE: California
 COUNTRY: US
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/648,322
 FILING DATE:
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: 519.0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-2937
 TELEFAX: (619) 554-6312
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 109 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-648-322-5

Query Match 13.3%; Score 79.5; DB 3; Length 109;
 Best Local Similarity 31.2%; Pred. No. 0.014;
 Matches 30; Conservative 4; Mismatches 35; Indels 27; Gaps 4;

Qy 37 LLQRALAAALPHRGVSEWRRTFYPNCPLR-----TFYPNCPLRW-----RPRKVKG 75
 Db 19 LLWGVASALPIESGPTGDSQVEATEGRSGLTF-----LAWWHEWAQSASSSTPVG 72

Qy 76 PQLKAKEDLERSVDNLPPRERKAGCKKNFYGFTSC 111
 Db 73 GTPGLSKSQERPPQQPPHLDKKPCRNFFWKTTPSSC 108

RESULT 7
 Sequence 7, Application US/08648322
 Patent No. 6074872

GENERAL INFORMATION:
 APPLICANT: Sutcliffe, Gregor J.
 APPLICANT: de Lecea, Luis
 TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES, COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
 STREET: 10666 No. 6074872nd Torrey Pines Road, TPC-8
 CITY: La Jolla
 STATE: California
 COUNTRY: US
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/648,322
 FILING DATE:
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: 519.0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-2937
 TELEFAX: (619) 554-6312
 INFORMATION FOR SEQ ID NO: 7
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: C-terminal
 US-08-648-322-7

Query Match 13.1%; Score 78; DB 3; Length 29;
 Best Local Similarity 51.9%; Pred. No. 0.0035;
 Matches 14; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 85 ERSVDNLPPRERKAGCKNFKYWKGFTSC 11.1
 Db 2 ERPLQQPPHRDKKPKCKNFFWKTFSSC 28

RESULT 8
 US-08-648-322-11

Sequence 11, Application US/08648322
 Patent No. 6074872

GENERAL INFORMATION:

APPLICANT: Sutcliffe, Gregor J.
 APPLICANT: de Lecea, Luis
 TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES, COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
 STREET: 10666 No. 6074872nd Torrey Pines Road, TPC-8
 CITY: La Jolla
 STATE: California
 COUNTRY: US
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/648,322
 FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: 519.0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-2937
 TELEFAX: (619) 554-6312
 INFORMATION FOR SEQ ID NO: 10
 SEQUENCE CHARACTERISTICS:
 LENGTH: 84 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: C-terminal
 US-08-648-322-10

Query Match 13.1%; Score 78; DB 3; Length 29;
 Best Local Similarity 51.9%; Pred. No. 0.0035;
 Matches 14; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 85 ERSVDNLPPRERKAGCKNFKYWKGFTSC 11.1
 Db 2 ERPLQQPPHRDKKPKCKNFFWKTFSSC 28

RESULT 9
 US-08-648-322-10

Sequence 10, Application US/08648322
 Patent No. 6074872

GENERAL INFORMATION:

APPLICANT: Sutcliffe, Gregor J.
 APPLICANT: de Lecea, Luis
 TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES, COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
 STREET: 10666 No. 6074872nd Torrey Pines Road, TPC-8
 CITY: La Jolla
 STATE: California
 COUNTRY: US
 ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/648,322
 FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: 519.0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-2937
 TELEFAX: (619) 554-6312
 INFORMATION FOR SEQ ID NO: 11
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: C-terminal
 US-08-648-322-11

Qy 85 ERSVDNLPPRERKAGCKNFWKGFTSC 111
 US-08-455-970A-10
 Sequence 10, Application US/08455970A
 Patent No. 5708155

Db 57 ERPPQQPPHLDKKCKNFFWRTFSSC 83

RESULT 10 US-08-455-970A-10

Sequence 10, Application US/08455970A

Patent No. 5708155

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: REDMOND, MARK J.

APPLICANT: HUGHES, HUW P.A.

TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 285 HAMILTON AVENUE, SUITE 200

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPILER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,970A

FILING DATE: 31-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 327-3400

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 943 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-455-970A-10

ADDRESSEE: Allegretti & Witcoff, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606

COMPILER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/977,628A
 FILING DATE: 17-NOV-1992

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 5405597nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 91,642-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEFAX: 312-715-1234
 TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 1:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 2..14
 OTHER INFORMATION: /label= Disulfide-bond
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 12 US-08-255-272-5
 Sequence 5, Application US/08255272
 Patent No. 5627268

GENERAL INFORMATION:
 Best Local Similarity 85.7%; Pred. No. 0.0018;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 98 AGCKNFWKGFTSC 111
 Db 1 AGCKNFFWKFTFTSC 14

RESULT 12 US-08-255-272-5
 Sequence 5, Application US/08255272
 Patent No. 5627268

GENERAL INFORMATION:
 Best Local Similarity 85.7%; Pred. No. 0.0018;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 98 AGCKNFWKGFTSC 111
 Db 1 AGCKNFFWKFTFTSC 14

RESULT 11 US-07-977-628A-1
 Sequence 1, Application US/07977628A
 Patent No. 5405597

GENERAL INFORMATION:
 APPLICANT: Dean, Richard T
 APPLICANT: Lister-James, John
 APPLICANT: Buttram, Scott
 TITLE OF INVENTION: Technetium-99m Labeled Somatostatin-Derived Peptides for Imaging

NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:

APPLICATION NUMBER: US/08/255,272
 FILING DATE: 4/35
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30742
 REFERENCE/DOCKET NUMBER: 6794-0322
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-255-272-5

Query Match 12.9%; Score 77; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 0.0018;
 Matches 12; Conservative 1; Indels 0; Gaps 0;
 QY 98 AGCKNFWKGFTSC 111
 Db 1 AGCKNFWKGFTSC 14

RESULT 13
 US-08-416-007-4
 Sequence 4, Application US/08416007
 Patent No. 5693679
 GENERAL INFORMATION:
 APPLICANT: Vincent, Jean-Pierre
 APPLICANT: Gaudriault, Georges
 APPLICANT: Beaudet, Alain
 TITLE OF INVENTION: FLUORESCENT SOMATOSTATIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/676,263
 FILING DATE: 07-NOV-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94300224.6
 FILING DATE: 12-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharp, Jeffrey S.
 REGISTRATION NUMBER: 31,879
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: (312) 474-6600
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Cross-links
 LOCATION: 3..14
 US-08-676-263-11

Query Match 12.9%; Score 77; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 0.0018;
 Matches 12; Conservative 1; Indels 0; Gaps 0;
 QY 98 AGCKNFWKGFTSC 111
 Db 1 AGCKNFWKGFTSC 14

RESULT 15
 US-08-286-748B-13
 Sequence 13, Application US/08286748B
 Patent No. 5759542

GENERAL INFORMATION:
APPLICANT: Victor Gurewich
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
OF DRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,748B

FILING DATE: August 5, 1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: J. Peter Fasse

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 04547/013001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 14

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-286-748B-13

Query Match 12.9%; Score 77; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 0.0018;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 98 AGCKNFWKGTSC 111
1 AGCKNFWKFTSC 14

Search completed: June 13, 2002, 12:22:56
Job time: 194 sec

Db 61 PNCPC1 - RPRKVCP - AGAKEDLRLVELERSVGPNPNNPRERKAGCKNFWKGFTSC 115

RESULT 2

ID SMS2_CARAU STANDARD; PRT; 120 AA.

AC Q9YGH4; Q9PTU2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Somatostatin II precursor [Contains: [Tyr7, Gly10] somatostatin-14].

OS Lophius americanus (American goosefish) (Anglerfish)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius.

OS Carassius auratus (Goldfish)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

OC Cypriniformes; Cyprinidae; Carassius.

[1] OX NCBI_TaxID=8073;

RN [1] RQ SEQUENCE FROM N.A.

RX MEDLINE-81052423; PubMed-6107860;

RX Hobart P.M., Crawford R., Shen L., Pictet R., Rutter W.J.;

RX "Cloning and sequence analysis of cDNAs encoding two distinct somatostatin precursors found in the endocrine pancreas of anglerfish.";

RX Nature 288:137-141(1980).

[2] RQ PARTIAL SEQUENCE, AND HYDROXYLATION.

RX MEDLINE-87308304; PubMed-2887572;

RX Andrews P.C., Nichols R., Dixon J.E.;

RX "Post-translational processing of preprosomatostatin-II examined using fast atom bombardment mass spectrometry.";

RL J. Biol. Chem. 262:12692-12699(1987).

CC -- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.

CC -- SUBCELLULAR LOCATION: Secreted.

CC -- MISCELLANEOUS: SOMATOSTATIN II MAY HAVE A DIFFERENT DEGREE OF ACTIVITY OR A DIFFERENT TYPE OF TARGET CELL FROM SOMATOSTATIN I.

CC -- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.

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CC DR EMBL; V00641; CAA23987.1; -

CC DR PIR; A01434; RIAFS2;

CC DR InterPro; IPR004250; Somatostatin.

CC DR Pfam; PF03002; Somatostatin; 1.

CC KW Cleavage on pair of basic residues: Hormone; Signal; Hydroxylation; Multigene family.

CC FT PROPEP 1 24 POTENTIAL.

CC FT PEPTIDE 25 109 [Tyr7, Gly10] somatostatin-14.

CC FT DISULFID 112 125 [Tyr7, Gly10] somatostatin-14.

CC FT DISULFID 114 125 HYDROXYLATION.

CC FT MOD_RES 120 120 DV -> TG (IN REF. 1).

CC FT CONFLICT 77 78 G -> E (IN REF. 1).

CC FT CONFLICT 90 90 SEQUENCE 125 AA; 14052 MW; 5E14605D7B9A46FE CRC64;

CC DR EMBL; U60262; AAD09626.1; -

CC DR AF025686; AAF15306.1; -

CC DR InterPro; IPR004250; Somatostatin.

CC DR Pfam; PF03002; Somatostatin; 1.

CC KW Multigene family.

CC FT SIGNAL 1 23 POTENTIAL.

CC FT PROPEP 24 92 [Tyr21, Gly24] somatostatin-28.

CC FT PEPTIDE 93 120 [Tyr7, Gly10] somatostatin-14.

CC FT DISULFID 107 120 BY SIMILARITY.

CC FT DISULFID 109 120 Q -> RW (IN REF. 2).

CC FT CONFLICT 51 51 SEQUENCE 120 AA; 13723 MW; 98957D68011A651A CRC64;

CC FT CONFLICT 55 42.08; Score 205.5; DB 1; Length 120; Pred. No. 2.6e-15; Mismatches 14; Indels 31; Gaps 7; Query Match 34.4%; Score 205.5; DB 1; Length 120; Mismatches 14; Indels 31; Gaps 7; Best Local Similarity 42.08; Score 205.5; DB 1; Length 120; Mismatches 14; Indels 31; Gaps 7; Query Match 34.4%; Score 205.5; DB 1; Length 120; Mismatches 14; Indels 31; Gaps 7; Best Local Similarity 39.7%; Pred. No. 1.6e-13; Mismatches 52;保守型 13; Indels 32; Gaps 7;

QY 1 MRYSQIHCALALLGLALAICSGQAASQ--PDLDLASRRLQRLAAALPHRSGVSERWRT 58

Db 1 MRLCELHCYLLGLGSLVLCGRANSQLEPDLDERRHRLLQRA---SATGQATQD 52

QY 59 FYP-----NCPC1LWRPRKVKGPQLKAK-EDL---ERSVDN---LPPRERKAGC 100

Db 53 FTKRDVEKLLSLISPEMRE--KGLSMAGESEDRLQERSAESSNQLPTRLRKEGC 109

QY 101 KNEYWKGF1TSC 111

Db 110 KNEYWKGF1TSC 120

QY 101 KNEYWKGF1TSC 111

Db 59 WSKRAVEELLAQMSLPEADV---QREAEDASMATGGRMNLERSVSDTNNLPRERKAGC 114

RESULT 4

ID SMS_CHICK STANDARD; PRT; 116 AA.

AC P33094; (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-OCT-1993 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Somatostatin precursor [Contains: Somatostatin-14].

GN Gallus gallus (Chicken).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.

NCBI_TAXID=7957;

RN SEQUENCE FROM N.A.

RP TISSUE=Brain;

RA Lin X.-W.; Peter R.E.; "Cloning and characterization of cDNAs encoding preprosomatostatin-I and -II from goldfish brain."

RT Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.

-I- SUBCELLULAR LOCATION: Secreted.

-I- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.

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CC EMBL; U40754; AAD09359.1;

CC DR InterPro; IPR004250; Somatostatin.

CC DR Pfam; PF03002; Somatostatin; 1.

CC KW Cleavage on pair of basic residues; Hormone; Signal; Multigene family.

CC FT SIGNAL 1 24 POTENTIAL.

CC FT PROPEP 25 88 POTENTIAL.

CC FT PEPTIDE 89 114 SOMATOSTATIN-26 (POTENTIAL).

CC FT PEPTIDE 101 114 SOMATOSTATIN-14.

CC FT DISULFID 103 114 BY SIMILARITY.

CC SQ SEQUENCE 114 AA; 12574 MW; B5920015E2D272A4 CRC64;

Query Match 29.9%; Score 178.5; DB 1; Length 114;

Best Local Similarity 38.2%; Pred. No. 2e-12;

Matches 50; Conservative 15; Mismatches 29; Indels 37; Gaps 5;

QY 1 MRVSQLCALIGLALICSGOGAASQPDLDLASRRLQLRALARAAALPHRSGVSERWRFTY 60

Db 1 MLSTRIQCALALLSIALAVCSVSA---PTDAKLRLQLQRSLL---NPAGKOE---- 47

QY 61. PNCPCLWRPRKVKGPQLKAK---EDLERSVDN----LPPRERKAGC 100

Db 48 ---LARYTLADLILSPELRSRAVELERAAGPMLAPRERKAGC 103

QY 101 KNFYWKFTSC 111

Db 104 KNFFWKFTSC 114

RESULT 6

SMS_HUMAN STANDARD; PRT; 116 AA.

ID SMS_HUMAN

AC P01166;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].

GN Homo sapiens (Human), and

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TAXID=9606, 9541;

RN SEQUENCE FROM N.A.

RC SPECIES=Human;

RX MEDLINE-84146798; PubMed-6142531;

RA Shen L.-P.; Rutter W.J.;

RESULT 5

ID SMSA_CARAU STANDARD; PRT; 114 AA.

AC Q9YGH5;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Somatostatin IA precursor [Contains: Somatostatin-26; Somatostatin-

"Sequence of the human somatostatin 1 gene.";
Science 224:168-171(1984).
[2]

SEQUENCE FROM N.A.
SPECIES=Human;
MEDLINE=83014931; PubMed=6126875;
RA Shen L.-P.; Pictet R.L.; Rutter W.J.;
RT "Human somatostatin 1: sequence of the cDNA";
RL Proc. Natl. Acad. Sci. U.S.A. 79:4575-4579(1982).
RN [3]

SEQUENCE FROM N.A.
SPECIES=M.fascicularis;
MEDLINE=88144503; PubMed=2894033;
RA Travis G.H.; Sutcliffe J.G.;
RT "Phenol emulsion-enhanced DNA-driven subtractive cDNA cloning:
isolation of low-abundance monkey cortex-specific mRNAs.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1696-1700(1988).
CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PHARMACEUTICAL: Available under the name Sandostatin (Novartis);
CC this is a synthetic cyclic analog known as octreotide or SMS
201-995. Used for the treatment of a variety of disorders
CC including acromegaly and the symptomatic treatment of carcinoid
CC tumors and vasoactive intestinal peptide tumors.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
CC
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CC
CC DR EMBL; J00306; AAA6056.1; -.
CC DR EMBL; M19318; AAA36908.1; -.
CC DR Pfam; PF03002; Somatostatin; 1.
CC DR PIR; A43614; RIHUS1.
CC DR PIR; A28968; A28968.
CC DR MIM; 182450;
CC DR InterPro; IPR004250; Somatostatin.
CC DR Pfam; PF03002; Somatostatin; 1.
CC KW Cleavage on pair of basic residues; Hormone; Multigene family; Signal.
CC FT SIGNAL. 1 24
CC FT PROPEP 25 88
CC FT PEPTIDE 89 116 SOMATOSTATIN-28.
CC FT PEPTIDE 103 116 SOMATOSTATIN-14.
CC FT DISULFID 105 116
CC SEQUENCE 116 AA; 12735 MW; AB49BB89DC9DD8DA CRC64;

Query Match 29.6%; Score 174; DB 1; Length 115;
Best Local Similarity 38.2%; Pred. No. 3.3e-12;
Matches 47; Conservative 19; Mismatches 30; Indels 27; Gaps 6;

Qy 5 QIHCALALLGLALAI-CSQGAASQPDLDLASSRLLQRALAAALPHRSGVSERWRTEYPNC 63
Db 5 RLQCALAALSIVLALGCVTGPASDPLR---RQFLQKSAAA---AGKQELAKYFLAE- 55

Query Match 29.1%; Score 174; DB 1; Length 115;
Best Local Similarity 39.4%; Pred. No. 6.1e-12;
Matches 50; Conservative 17; Mismatches 32; Indels 28; Gaps 6;

Qy 1 MRVSOIHCALALLGLALAI-CSQGAASQPDLDLASSRLLQRALAAALPHRSGVSERWRTE 59
Db 1 MQSCRVQCALTLLSALAINSSAAPTDPRL---RQFLQKSAAA---GKQELAKYF 51

Query Match 29.1%; Score 174; DB 1; Length 115;
Best Local Similarity 39.4%; Pred. No. 6.1e-12;
Matches 50; Conservative 17; Mismatches 32; Indels 28; Gaps 6;

Qy 60 YPNCPCLRWRPRKVKGPQLKAKE-----DLERSVDNLPL---PRERKAGCKKNFY 104
Db 52 LAE---LLSEPSQTDNEALESDDLPRGAAEQDEVRLELERSANSNPAMAPRERKAGCKKNFY 108

Query Match 29.1%; Score 174; DB 1; Length 115;
Best Local Similarity 39.4%; Pred. No. 6.1e-12;
Matches 50; Conservative 17; Mismatches 32; Indels 28; Gaps 6;

Qy 105 WKGFTSC 111
Db 109 WKGFTSC 115

RESULT 7
SMS1_RANRI
ID SMS1_RANRI STANDARD PRT; 115 AA.
AC P87384; Q9PSI8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

RESULT 8
SMS_SHEEP
ID SMS_SHEEP STANDARD PRT; 116 AA.
AC O46688;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].
GN SST.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
NCBI_TaxID=940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN="ILE DE FRANCE";
RX MEDLINE=99094691; PubMed=9880082;
RA Bruneau G., Tillet Y.;
RT "Localization of the preprosomatostatin-mRNA by *in situ* hybridization
in the ewe hypothalamus.";
RT Peptides 19:1749-1758(1998).
RL 1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
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or send an email to license@isb-sib.ch).
CC DR EMBL; AF031488; AAC04697.1;
DR EMBL; Y15267; CAA75556.1;
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin; 1.
DR KW Cleavage on pair of basic residues; Hormone; Signal.
FT SIGNAL 1 24 BY SIMILARITY.
FT PROPEP 25 88 BY SIMILARITY.
FT PEPTIDE 89 116 SOMATOSTATIN-28.
FT PEPTIDE 103 116 SOMATOSTATIN-14.
FT DISULFID 105 116 BY SIMILARITY.
SQ SEQUENCE 116 AA; 12689 MW; C18F17E31A3718DE CRC64;

Query Match 27.9%; Score 166.5; DB 1; Length 116;
Best Local Similarity 37.4%; Pred. No. 4e-11;
Matches 46; Conservative 19; Mismatches 31; Indels 27; Gaps 6;

Qy 5 QIHCALALLGLALAICS-QGAASQPDLDDASRRLQLRALARALPHRSGVSEWRWTFYPCN 63
Db 5 RLIQCALAALSIVLALGGVTGAPSPDPRL---RQFLQKSAA---AGKQELAKYFLAE- 55

Qy 64 PCLRWPRPKVKGPQLKAE-----DLERSVDNLPL---PRERKAGCKNPKYWKGF 108
Db 56 -LLSEPNOTDALEPEPDLSQAAEQDEMRLQRSANSNPAMAPRERKAGCKNFEFWKTF 113

Qy 109 TSC 111
Db 114 TSC 116

RESULT 9
SMS_MOUSE STANDARD; PRT; 116 AA.
ID SMS_MOUSE
AC P01167;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin precursor [Contains: Antrin; Somatostatin-28;
DE Somatostatin-14].
GN SST OR SMST.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090, 10116;

RN SEQUENCE FROM N.A.
RP SPECIES=Rat;
RC MEDLINE=83238516; PubMed=6134734;
RX MEDLINE=83213516; PubMed=6133871;
RA Argos P., Taylor W.L., Minth C.D., Dixon J.E.;
RT "Nucleotide and amino acid sequence comparisons of
preprosomatostatins";
RT J. Biol. Chem. 258:8788-8793(1983).
RN [2]
RN SEQUENCE FROM N.A.
RP SPECIES=Rat;
RC MEDLINE=83213516; PubMed=6133871;
RX Goodman R.H., Aron D.C., Roos B.A.;
RA "Rat pre-prosomatostatin. Structure and processing by microsomal
membranes.";
RT J. Biol. Chem. 258:5570-5573(1983).
RN [3]
RN SEQUENCE FROM N.A.
RP SPECIES=Rat;
RC MEDLINE=85303584; PubMed=2863939;
RX Goodman R.H., Montminy M.R., Low M.J., Habener J.F.;
RA "Biosynthesis of rat preprosomatostatin.";
RT Adv. Exp. Med. Biol. 188:31-47(1985).
RN [4]
RN SEQUENCE FROM N.A.
RP SPECIES=Rat;
RC MEDLINE=84221954; PubMed=6145156;
RX Goodman R.H., Jacobs J.W., Horovitz S.J., Habener J.F.;
RA Montminy M.R., Goodman R.H., Horovitz S.J., Habener J.F.;
RT "Primary structure of the gene encoding rat preprosomatostatin.";
RT Proc. Natl. Acad. Sci. U.S.A. 81:3337-3340(1984).
RN [5]
RN SEQUENCE FROM N.A.
RP SPECIES=Rat;
RC MEDLINE=84221954; PubMed=6145156;
RX Goodman R.H., Jacobs J.W., Dee P.C., Habener J.F.;
RA Montminy M.R., Goodman R.H., Horovitz S.J., Habener J.F.;
RT "Somatostatin-28 encoded in a cloned cDNA obtained from a rat
medullary thyroid carcinoma";
RT J. Biol. Chem. 257:1156-1159(1982).
RN [6]
RN SEQUENCE OF 38-116 FROM N.A.
RP SPECIES=Rat;
RC MEDLINE=82120034; PubMed=6120163;
RX Goodman R.H., Jacobs J.W., Dee P.C., Habener J.F.;
RA Montminy M.R., Goodman R.H., Horovitz S.J., Habener J.F.;
RT "Somatostatin-28 encoded in a cloned cDNA obtained from a rat
medullary thyroid carcinoma";
RT J. Biol. Chem. 257:1156-1159(1982).
RN [7]
RN SEQUENCE OF 25-34.
RP SPECIES=Rat; STRAIN=SPRAGUE-DAWLEY;
RC MEDLINE=88070564; PubMed=2891188;
RX Benoit R., Ling N., Esch F.;
RA "A new prosomatostatin-derived peptide reveals a pattern for
hormone cleavage at monobasic sites.";
RT J. Biol. Chem. 238:1126-1129(1987).
RN [8]
RN SEQUENCE FROM N.A.
RP SPECIES=Mouse; TISSUE=Brain;
RC MEDLINE=90206793; PubMed=11969620;
RX Fuhrmann G., Heiling R., Kampf J., Ebel A.;
RT "Nucleotide sequence of the mouse preprosomatostatin gene.";
RL Nucleic Acids Res. 18:1287-1287(1990).
CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
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DR EMBL; K02248; AAA42161.1; -.
 DR EMBL; V01271; CAA24579.1; -.
 DR EMBL; J00787; AAA42164.1; -.
 DR EMBL; M25890; AAA42167.1; -.
 DR EMBL; J00788; AAA42162.1; -.
 DR EMBL; X51468; CAA35831.1; -.
 DR PIR; A20983; RIRTS1.
 DR PIR; S08416; S08416.
 DR MGI; 98326; Smst.
 DR InterPro; IPR004250; Somatostatin.
 Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL; 1 24; FT SIGNAL; 1 24; BY SIMILARITY.
 FT PEPTIDE; 25 34; FT PROPEP; 25 88; BY SIMILARITY.
 FT PEPTIDE; 35 88; FT PEPTIDE; 89 116; SOMATOSTATIN-28.
 FT PEPTIDE; 89 116; FT PEPTIDE; 103 116; SOMATOSTATIN-14.
 FT PEPTIDE; 103 116; FT PEPTIDE; 105 116; BY SIMILARITY.
 FT DISULFID; 105 116; FT DISULFID; 105 116; BY SIMILARITY.
 FT CONFICT; 43 43; T > Y (IN REF. 5).
 FT CONFICT; 79 79; Q > H (IN REF. 6).
 FT SEQUENCE; 116 AA; 12745 MW; D48B5454C4490375 CRC64;

Query Match 27.4%; Score 163.5; DB 1; Length 116;
 Best Local Similarity 37.4%; Pred. No. 8.3e-11; Mismatches 6;
 Matches 46; Conservative 19; Indels 27; Gaps 6;

QY 5 QIHCALALLGLALAICS-QGAASQPDDLQLASRRLQLQRALAAALPHRSGVSERWRPFYPCNC 63
 Db 5 RLOCALANLCIVLALGGVTGAPSDPRL---RQFLQKSIAAA---TGKQELAKYFLAE- 55
 QY 64 PCLRWRPKVKKGPKQLKAKE---DLERSVDNLP---PRERKAGCKKNFYWKGF 108
 Db 56 --LLSEPNQTEIDALEPEDLSQAAEQDEMRLQRSANSNPAMA PRERKAGCKKNFWKTF 113
 QY 109 TSC 111
 Db 114 TSC 116

RESULT 10

SMS_BOVIN STANDARD; PRT; 116 AA.
 ID P26917; AC P49670; DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].
 SST. [1] Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TAXID=9913;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE-88288237; PubMed-2899837;
 RA Su C.J., White J.W., Li W.H., Luo C.C., Frazier M.L., Saunders G.F., Chan L.; RT "structure and evolution of somatostatin genes.";
 RT Mol. Endocrinol. 2:209-216(1988).
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN-HOLSTEIN; MEDLINE=99196780; PubMed=10100681;
 RX Furu L.M., Kazmer G.W., Strausbaugh L., Zinn S.A.; RT "Cloning and characterization of the bovine somatostatin gene.";
 RL J. Anim. Sci. 77:492-493(1999).

CC - - FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC - - SUBCELLULAR LOCATION: Secreted.
 CC - - SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
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CC DR EMBL; M31217; AAA30744.1;
 DR EMBL; U97077; AAB58056.1; -.
 DR PIR; A40929; A40929.
 DR InterPro; IPR004250; Somatostatin.
 Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL; 1 24; FT SIGNAL; 1 24; BY SIMILARITY.
 FT PROPEP; 25 88; BY SIMILARITY.
 FT PEPTIDE; 89 116; SOMATOSTATIN-28.
 FT PEPTIDE; 103 116; SOMATOSTATIN-14.
 FT DISULFID; 105 116; BY SIMILARITY.
 SQ SEQUENCE 116 AA; 12688 MW; C18F17E64A371D8E CRC64;

Query Match 27.2%; Score 162.5; DB 1; Length 116;
 Best Local Similarity 37.4%; Pred. No. 1.1e-10;
 Matches 46; conservative 19; Mismatches 31; Indels 27; Gaps 6;

QY 5 QIHCALALLGLALAICS-QGAASQPDDLQLASRRLQLQRALAAALPHRSGVSERWRPFYPCNC 63
 Db 5 RLOCALANLCIVLALGGVTGAPSDPRL---RQFLQKSIAAA---TGKQELAKYFLAE- 55
 QY 64 PCLRWRPKVKKGPKQLKAKE---DLERSVDNLP---PRERKAGCKKNFYWKGF 108
 Db 56 --LLSEPNQTEIDALEPEDLSQAAEQDEMRLQRSANSNPAMA PRERKAGCKKNFWKTF 113
 QY 109 TSC 111
 Db 114 TSC 116

RESULT 11

SMS_CANFA STANDARD; PRT; 116 AA.

ID SMS_CANFA AC P49670; DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].
 SST. [1] Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TAXID=9615;
 RN SEQUENCE FROM N.A.
 RC TISSUE=Gastric mucosa;
 RX MEDLINE=97142297; PubMed=8988514;
 RA Dickinson C.J., Delvalle J., Todisco A., Gantz I., Tong L.,
 RA Finniss S., Yamada T.; RT "Canine prosomatostatin: isolation of a cDNA, regulation of gene
 expression, and characterization of post-translational processing
 intermediates.";
 RT Requi. Pept. 67:145-152(1996).
 RL Mol. Endocrinol. 2:209-216(1988).
 CC - - FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC - - SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
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CC EMBL: AF126243; AAD39138.1;
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin.
 CC KW Cleavage on pair of basic residues; Hormone: Multigene family: Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT PROPEP 25 88 POTENTIAL.
 FT PEPTIDE 89 115 SOMATOSTATIN-27 (POTENTIAL).
 FT PEPTIDE 102 115 SOMATOSTATIN-14.
 FT DISULFID 104 115 BY SIMILARITY.
 SQ SEQUENCE 115 AA; 12600 MW; B0CEF1E603FEAF09 CRC64;

Query Match 25.6%; Score 153; DB 1; Length 115;
 Best Local Similarity 38.3%; Pred. No. 1.1e-09;
 Matches 46; Conservative 13; Mismatches 39; Indels 22; Gaps 5;

5 QIHCALALLGLALAICSGQAASQPDLQLASRQLLQLRALAALPHRGSGVSEWRFTYPNCP 64
 ||| :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 5 RFQCALVVLSSLAVFESKVSAAPS --DLRLRQLLQLRSLAAAGKQE-LTKYSLAE 55
 Db 65 CLRWRPRKVK-----GPQLKAKEDLERSVDSLNP--PRERKAGCKNFKYWKGFTSC 111
 | : :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 56 LLSELAQSENDALDSSDLRGADQDEVRLDRSANSPLAARERKAGCKNFKWFTFTSC 115

RESULT 14.
 SMS2_PLAFe STANDARD; PRT; 73 AA.
 AC P21780;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin II precursor [Contains: [Tyr21, Gly24] somatostatin-28];
 DE [Tyr7, Gly10] somatostatin-14 (Fragments).
 OS Platichthys flesus (European flounder).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Pleuronectoidei; Pleuronectidae; Platichthys.
 OX NCBI_TAXID=8260;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=88029486; PubMed=2889597;
 Conlon J.M., Davis M.S., Falkmer S., Thim L.;
 "Structural characterization of peptides derived from
 prosomatostatins I and II isolated from the pancreatic islets of two
 species of teleostean fish: the daddy sculpin and the flounder.";
 RL Eur. J. Biochem. 168:647-652(1987).
 CC -I- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 DR PIR; S00169; S00169.
 KW Cleavage on pair of basic residues; Hormone: Multigene family.
 FT NON_TER 1 1
 FT NON_CONS 10 11
 FT NON_CONS 45 46
 FT PEPTIDE 46 73 [TYR21, GLY24] SOMATOSTATIN-28.
 FT PEPTIDE 60 73 [TYR7, GLY10] SOMATOSTATIN-14.
 FT DISULFID 62 73 CCCBA6B30DCB29BB CRC64;
 SQ SEQUENCE 73 AA; 7989 MW;

Query Match 22.8%; Score 136; DB 1; Length 73;
 Best Local Similarity 51.9%; Pred. No. 4.6e-08;
 Matches 27; Conservative 4; Mismatches 5; Indels 16; Gaps 2;

Query Match 76 PQLKAKEDLERSVDSLNP--PRERKAGCKNFKYWKGFTSC 111
 | : :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

22 PEADAQRDAENVSTATGGGRMNQESIEPPNNLPPRERKAGCKNFKYWKGFTSC 73
 RESULT 15.
 SMS_PIG STANDARD; PRT; 92 AA.
 ID SMS_PIG
 AC P01168;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-Oct-2001 (Rel. 40, Last annotation update)
 DE Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14]
 DE (Fragment).
 GN OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TAXID=9823;
 RN SEQUENCE OF 1-64.
 RP PubMed=2567292;
 RX MEDLINE=89278131;
 RA Bersani M., Thim L., Baldissara F.G.A., Holst J.J.;
 "Prosomatostatin 1-64 is a major product of somatostatin gene
 expression in pancreas and gut.";
 RT J. Biol. Chem. 264:10633-10636(1989).
 RL [2]
 RN SEQUENCE OF 1-32.
 RP PubMed=2865169;
 RX MEDLINE=86030691;
 RA Schmidt W.E., Mutt V., Kratzin H., Carlquist M., Conlon J.M.,
 Creutzfeldt W., "Isolation and characterization of proSS1-32, a peptide derived from
 the N-terminal region of porcine preprosomatostatin.";
 RT FEBS Lett. 192:141-146(1985).
 RL [3]
 RN SEQUENCE OF 65-92.
 RP PubMed=6107906;
 RX TISSUE=Intestine;
 MEDLINE=80113258; PubMed=7353633;
 RA Pradayrol L., Joernvall H., Mutt V., Ribet A.;
 "N-terminally extended somatostatin: the primary structure of
 somatostatin-28.";
 RT FEBS Lett. 109:55-58(1980).
 RL [4]
 RN SEQUENCE OF 65-92.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=81054799; PubMed=6107906;
 RA Schally A.V., Huang W.-Y., Chang R.C.C., Arimura A., Redding T.W.,
 Millar R.P., Hunkapiller M.W., Hood L.E.;
 "Isolation and structure of pro-somatostatin: a putative somatostatin
 precursor from pig hypothalamus.";
 RT Proc. Natl. Acad. Sci. U.S.A. 77:4489-4493(1980).
 RL [5]
 RN SEQUENCE OF 79-92.
 RX MEDLINE=76136331; PubMed=1252409;
 RA Schally A.V., Dupont A., Arimura A., Redding T.W., Nishi N.,
 Lintthicum G.L., Schlesinger D.H.;
 "Isolation and structure of somatostatin from porcine hypothalamus.";
 RL Biochemistry 15:509-514(1976).
 RL [6]
 RN SEQUENCE OF 22-92 FROM N.A.
 RP Riquet J.;
 CC Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
 CC -I- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -I- SUBCELLULAR LOCATION: Secreted.
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EMBL; U36385; AAB38485.1; -

DR

DRR	PIR; A01432; RIPGS.	Query Match	22.88;	Score	136;	DB	1;	Length
DRR	PIR; A24222; A24222.	Best Local Similarity	36.98;	Pred.	No.	5.9e-08;		
DRR	PIR; A34109; A34109.	Matches	38;	Conservative	15;	Mismatches	24;	Inde
DRR	PIR; S13616; S13616.							
DRR	InterPro; IPR004250; Somatostatin.							
DRR	Pfam; PF03002; Somatostatin; 1.							
KW	Cleavage on pair of basic residues; Hormone.							
FFT	NON_TER	1	1					
FFT	PROPEP	1	64	SOMATOSTATIN-28.				
FFT	PEPTIDE	65	92	SOMATOSTATIN-14.				
FFT	PEPTIDE	79	92					
DISULFID	DISULFID	81	92					
SEQUENCE	SEQUENCE	92	AA;	10346	MW;	787CBE82CFBBAE76	CRC64;	

Search completed: June 13, 2002, 12:29:54
Job time: 446 sec

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: June 13, 2002, 12:31:02 ; Search time 60.72 seconds

(without alignments)
31.340 Million cell updates/sec

Title: US-09-727-739B-18

Perfect score: 58

Sequence: 1 SVDNLPPRERK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_19:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Q9haa3 homo sapien
 Q9fyb0 arabidopsis
 Q972m6 sulfolobus
 Q9vqt3 drosophila
 Q9v7y5 drosophila
 Q9awj8 oryza sativ
 Q96jf7 homo sapien
 Q93v10 arabidopsis
 Q942337 arabidopsis
 Q9zqc9 arabidopsis
 Q91f10 arabidopsis
 Q9qpn0 bovine rota
 Q9rs2 arabidopsis
 Q9vcd6 drosophila
 Q99v03 staphylococ
 Q98511 gracilaria
 Q96b18 homo sapien
 Q15224 homo sapien
 Q9wsq6 apple chlor
 Q99v03 staphylococ
 Q98511 gracilaria
 Q96b18 homo sapien
 Q15224 homo sapien
 Q9tyw6 caenorhabdi
 Q9jxk2 neisseria m
 Q9jwc7 neisseria m
 Q916v5 pseudomonas
 Q58603 pyrococcus
 Q9wsq6 apple chlor
 Q9jxk2 neisseria m
 Q96qu1 homo sapien
 Q96qt8 homo sapien
 Q99aq4 tt virus o
 Q15107 homo sapien
 Q15108 homo sapien

ALIGNMENTS

RESULT: 1

Q90Y43 PRELIMINARY; PRT; 115 AA.
 ID Q90Y43; AC Q90Y43;
 DT 01-DEC-2001 (TREMBLREL. 19, Created);
 DT 01-DEC-2001 (TREMBLREL. 19, Last sequence update);
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update);
 DE PREPROSOMATOSTATIN.
 OS Osteoglossum bicirrhosum (silver arowana).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Osteoglossidae; Osteoglossum.
 NCBI_TAXID=109271;

RN [1] RP SEQUENCE FROM N.A.
 RA Al-Mahrouki A.A., Irwin D.M., Youson J.H.;
 RT "Characterization of variant somatostatin cDNAs from several
 osteoglossomorphs: molecular identification and comparative
 analysis";
 RT Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF292650; AAK07067.1;
 DR SEQ EMBL; AF292650; AAK07067.1;
 SQ SEQUENCE 115 AA; 12791 MW; D65FBDD7C6F1B4E4D CRC64;

RESULT: 2

Query Match 79.3%; Score 46; DB 13; Length 115;
 Best Local Similarity 80.0%; Pred. No. 0.59;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 SEQ Y 2 VDNLPPRERK 11
 Q9v466 PRELIMINARY;
 ID Q9v466
 AC Q9v466;
 DT 01-MAY-2000 (TREMBLREL. 13, Created);
 DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)

SUMMARIES

8

Result No.	Score	Query	Match	Length	DB	ID	Description
1	46	79.3	115	13	Q90Y43		Q90Y43 osteoglossu
2	46	79.3	845	5	Q9v466		Q9v466 drosophila
3	42	72.4	273	3	Q13787		O13787 schizosacch
4	41	70.7	114	13	Q90Y42		Q90Y42 pantodon bu
5	40	69.0	242	4	Q9Y3T1		Q9Y3T1 homo sapien
6	40	69.0	275	16	Q98BW0		Q98bw0 rhizobium 1
7	40	69.0	349	16	Q92WH3		Q92wh3 rhizobium m
8	40	69.0	368	17	Q97YY4		Q97yy4 sulfolobus
9	40	69.0	477	2	Q93BD1		Q93BD1 mycobacteri
10	40	69.0	962	5	Q9N6U5		Q9n6u5 drosophila
11	40	69.0	1006	5	Q9VTE2		Q9vte2 drosophila
12	39	67.2	219	10	Q9FQE4		Q9fqe4 glycine max
13	39	67.2	224	10	Q9FQD8		Q9fqd8 glycine max
14	39	67.2	444	16	Q9RX02		Q9rx02 delnoococcus
15	39	67.2	796	5	Q9VAP3		Q9vap3 drosophila
16	38	65.5	158	11	Q9CYE7		Q9cy7 mus musculu

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE BCDNA:LD18761 PROTEIN.
 GN BCDNA:LD18761 OR CG6743.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydrioidea; Drosophilidae; Drosophila; Drosophila; NCBI_TAXID-7227;
 [1].

RN RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S.E., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Abybayan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Beeson K.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Hernandez J.R., Hennandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 [2].

RP SEQUENCE FROM N.A.
 RA Tsang G., Brokstein P., Frise E., Harvey D., Evans-Holm M.,
 RA Lewis S.E., Suh C., Rubin G.M.;
 RT "Full Length *Drosophila melanogaster* cDNA sequence.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE003629; AAF53002.1;
 DR EMBL; AF160938; AAD46878.1;
 DR FlyBase; FBgn0027868; BCDNA:LD18761.1;
 SQ SEQUENCE 845 AA; 97381 MW; 0A75HB07A6AFD6B6 CRC64;

Query Match 79.3%; Score 46; DB 5; Length 845;
 Best Local Similarity 88.9%; Pred. No. 4.5;
 Matches 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVNDNLPPRE 9
 DB 641 SVDNIPPRE 649

RESULT 3
 O13787

DT 013787; PRELIMINARY; PRT; 273 AA.
 AC 013787; 08; Created
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PUTATIVE TRANSLLOCATION PROTEIN C17G6.09.
 GN SPAC17G6.09.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetidae;
 OC Schizosaccharomyctales; Schizosaccharomycetes;
 OC Schizosaccharomyces.
 OX NCBI_TAXID=4896;
 RN SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Murphy L., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
 RA Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 RL -I- FUNCTION: REQUIRED FOR PREPROTEIN TRANSLLOCATION (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -I- SIMILARITY: TO YEAST AND Y. LIPOLYTICA SEC62.
 DR EMBL; Z99162; CAB16220.1;
 DR Hypothetical protein; Protein transport; Translocation; Transmembrane; KW Endoplasmic reticulum.
 KW CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1 132
 FT TRANSMEM 133 153
 FT DOMAIN 153 167
 FT TRANSMEM 154 167
 FT TRANSMEM 168 210
 FT DOMAIN 211 273
 SQ SEQUENCE 273 AA; 31585 MW; EE7A6369530799B3 CRC64;

Query Match 72.4%; Score 42; DB 3; Length 273;
 Best Local Similarity 70.0%; Pred. No. 7.7;
 Matches 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VDNLPPRERK 11
 DB 93 VDKLPPQORK 102

RESULT 4
 Q90Y42 PRELIMINARY; PRT; 114 AA.
 TD Q90Y42
 AC Q90Y42;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PREPROSOMATOSTATIN.
 OS Pantodon buchholzi (Butterflyfish).
 OC Actinopterygii; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Osteoglossiformes; Pantodontidae; Pantodon.
 OC Pantodon buchholzi; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Eukaryota; Metazoa;
 RN SEQUENCE FROM N.A.
 RA Al-Mahrouk A.A., Irwin D.M., Youson J.H.;
 RT "Characterization of variant somatostatin cDNAs from several
 osteoglossomorphs: molecular identification and comparative
 analysis.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF292651; AAK97068.1;
 DR SEQUENCE 114 AA; 12352 MW; 7E3D44CB6A27B12F CRC64;

Query Match 70.7%; Score 41; DB 13; Length 114;
 Best Local Similarity 87.5%; Pred. No. 4.8;
 Matches 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NLPPRERK 11
 DB 93 NVPPRERK 100

RESULT 5
 ID Q9Y3T1; PRELIMINARY; PRT; 242 AA.
 AC Q9Y3T1; 12, Created
 DT 01-NOV-1999 (TREMBrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBrel. 12, Last annotation update)
 DE HYPOTHETICAL 28.3 KDa PROTEIN (FRAGMENT).
 GN DKFP564A063.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 JR EMBL; AL050008; CAB43235.1;
 KW HYPOTHETICAL PROTEIN.
 FT NON-TER
 SEQUENCE 242 AA; 28250 MW; 84DEC201625C3B1F CRC64;

Query Match 69.0%; Score 40; DB 4; Length 242;
 Best Local Similarity 72.7%; Pred. No. 16;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVNDNLPPRERK 11
 DB 145 SWDSLPPSERK 155

RESULT 6
 ID Q98BW0; PRELIMINARY; PRT; 275 AA.
 AC Q98BW0; 18, Created
 DT 01-OCT-2001 (TREMBrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBrel. 18, Last annotation update)
 DT 01-OCT-2001 (TREMBrel. 18, Last annotation update)
 DE MLR5406 PROTEIN.
 GN MLR5406.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 UN [1];
 RP SEQUENCE FROM N.A.
 RX STRAIN-MAFF303099; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti.
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003006; BAB51862.1;
 DR InterPro; IPR01763; Rhodanese_domain.
 DR SMART; SM00450; RHOD; 1.
 KW Complete proteome.
 SEQUENCE 275 AA; 30613 MW; E12618905C17D6E5_CRC64;

Query Match 69.0%; Score 40; DB 16; Length 275;
 Best Local Similarity 63.6%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVNDNLPPRERK 11
 DB 110 SRTDKLPPRDEK 120

Query Match	Score 40; DB 17; Length 368;	Pred. No. 24;	Best Local Similarity 60.0%;	Matches 4; Mismatches 0; Indels 0; Gaps 0;	RESULT 11
2 VDNLPPRERK 11 : : : :	PRELIMINARY; PRT; 477 AA.				Q9VTE2 PRELIMINARY; PRT; 1006 AA.
72 VDDLPPKDRR 81					Q9VTE2; AC 01-MAY-2000 (TREMBLrel. 13, Created)
					DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
					DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
RESULT 9					DE SUPPRESSOR OF UNDERREPLICATION ES-PROTEIN.
0938D1					GN SU(UR)ES OR CG7869.
					OS Drosophila melanogaster (Fruit fly).
					OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
					OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
					OC Ephydriidae; Drosophilidae; Drosophila.
					NCBI_TaxID=7227;
					[1]
					RN SEQUENCE FROM N.A.
					RC STRAIN-BERKELEY;
					RC MEDLINE=20196006; PubMed=10731132;
					RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
					RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
					RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
					RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
					RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champine M., Pfeiffer B.D.,
					RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
					RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
					RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
					RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
					RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
					RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
					RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
					RA Dietz S.M., Mays A.D., Dew I., Dietz Z., Dunn P.,
					RA de Pablos B., Delcher A., Deng Z., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
					RA Dodson K., Doup L.E., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
					RA Durbin R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
					RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
					RA Glodek A., Gong F., Gorrell J.H., Gu Z., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
					RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
					RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
					RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
					RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
					RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
					RA Mount S.M., Moy M., Murphy B., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pollard J., Puril V., Reese M.G.,
					RA Palazzolo M., Pittman G.S., Pan S., Saunders R.D.C., Scheeler F., Shem H., Reinert K., Remington K., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shue B.C., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svartska R., Tector C., Turner R., Venter E., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R. F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Gibb R.A., Myers E.W., Rubin G.M., Venter J.C.,
					RA The genome sequence of Drosophila melanogaster.;
					RA Science 287: 2185-2195 (2000).
					RL EMBL; AE003546; AAF50110.2;
					DR FlyBase; FBgn0025355; SU(UR)ES.
					DR InterPro; IPR000330; SNF2_N.
					DR Pfam; PF00176; SNF2_N; 1.
					SQ SEQUENCE 1006 AA; 112638 MW; C281A9520DD24D2A CRC64;
					Query Match 69.0%; Score 40; DB 5; Length 1006;
					Best Local Similarity 60.0%; Pred. No. 68;
					Matches 3; Mismatches 1; Indels 0; Gaps 0;
					QY 1 SVDNLPPRER 10

Db	444 ATDNMPKR 453	Qy	3 DNLPFR 10 ;	Prt;	219 AA.
	RESULT 12				
	Q9FQE4; PRELIMINARY;				
	TD 09FQE4; PRT; 219 AA.				
	AC Q9FQE4; PRELIMINARY;				
	DT 01-MAR-2001 (TREMBLrel. 16, Created)				
	DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
	DE GLUTATHIONE S-TRANSFERASE GST 14 (EC 2.5.1.18) (FRAGMENT)				
	OS Glycine max (Soybean)				
	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine				
	OC NCBITAXID-3847;				
	RN SEQUENCE FROM N.A.				
	RP MEDLINE-20532786; PubMed-11080288;				
	RA McGonigle B.; Keeler S.J.; Lau S.M.C.; Koeppe M.K.; O'Keeffe D.P.; RT "A Genomics Approach to the Comprehensive Analysis of the Glutathione S-Transferase Gene Family in Soybean and Maize.";				
	RT Plant Physiol. 124:1105-1120(2000).				
	RL EMBL; AF243369; AAG34804.1;				
	DR InterPro; IPR004046; GST_C.				
	DR InterPro; IPR004045; GST_N.				
	DR Pfam; PF00043; GST_C; 1.				
	KW Transferase.				
	FT NON_TER 1				
	SQ SEQUENCE 219 AA; 25356 MW; 7378601EFB6C7630 CRC64;				
	Query Match 67.2%; Score 39; DB 10; Length 219;				
	Best Local Similarity 75.0%; Pred. No. 22;				
	Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;				
	Qy 3 DNLPFR 10 ;				
	Db 194 DNLPFR 201				
	RESULT 13				
	Q9FQD8 PRELIMINARY;				
	TD 09FQD8; PRT; 224 AA.				
	AC Q9FQD8; PRELIMINARY;				
	DT 01-MAR-2001 (TREMBLrel. 16, Created)				
	DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
	DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)				
	DE GLUTATHIONE S-TRANSFERASE GST 20 (EC 2.5.1.18)				
	OS Glycine max (Soybean)				
	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine				
	OC NCBITAXID-3847;				
	RN SEQUENCE FROM N.A.				
	RP MEDLINE-20532786; PubMed-11080288;				
	RA McGonigle B.; Keeler S.J.; Lau S.M.C.; Koeppe M.K.; O'Keeffe D.P.; RT "A Genomics Approach to the Comprehensive Analysis of the Glutathione S-Transferase Gene Family in Soybean and Maize.";				
	RT Plant Physiol. 124:1105-1120(2000).				
	RL EMBL; AF243375; AAG34810.1;				
	DR InterPro; IPR004046; GST_C.				
	DR InterPro; IPR004045; GST_N.				
	DR Pfam; PF00043; GST_C; 1.				
	DR Pfam; PF02798; GST_N; 1.				
	KW Transferase.				
	SQ SEQUENCE 224 AA; 26222 MW; 013C0D0C72D630DF CRC64;				
	Query Match 67.2%; Score 39; DB 10; Length 224;				
	Best Local Similarity 75.0%; Pred. No. 22;				
	Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;				

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbanyi A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra L.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doupe L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell D., Heiman T.J., Hernandez J.R., Harris M.,
 RA Harris N.L., Harvey D., Houston K.A., Howland T.J., Hernández J.R., Houck J.,
 RA Hostin D., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*,"
 RL *Science* 287:2185-2195(2000).
 DR EMBL; AE003768; AAF56859.1;
 DR FLYBASE; FBgn0039637; CG111880.
 SQ SEQUENCE 796 AA; 90628 MW; 20961DD889A3EE3B CRC64;

Query Match 67.2%; Score 39; DB 5; Length 796;
 Best Local Similarity 66.7%; Pred. No. 82;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 DNLLPRERK 11
 Db 786 :111111:
 NNLPPRQRR 794

Search completed: June 13, 2002, 12:31:03
 DB time: 485 sec

SO SEQUENCE 125 AA; 14052 MW; 5E14605D7B9A46FE CRC64;

Query Match 84.5%; Score 49; DB 1; Length 125;
Best Local Similarity 81.8%; Pred. No. 0.027; 1; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 1; -

QY 1 SVDNLPPRERK 11
Db 101 STNNLPPRERK 111

RESULT 2

SMS2_PLAIE STANDARD; PRT; 73 AA.

ID SMS2_PLAIE STANDARD; PRT; 73 AA.

AC P21780;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-Oct-2001 (Rel. 40, Last annotation update)
DE Somatostatin II precursor [Contains: [Tyr21,Gly24]somatostatin-28;
[Tyr7,Gly10]somatostatin-14] (Fragments).
E Platichthys flesus (European flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorphi; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Platichthys.
NCBI_TaxID=8260;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas; MEDLINE=88029486; PubMed=2889597;
RA Conlon J.M., Davis M.S., Falkmer S., Thim L.;
RT "Structural characterization of peptides derived from prosomatostatins I and II isolated from the pancreatic islets of two species of teleostean fish: the daddy sculpin and the flounder.";
RU Eur. J. Biochem. 168:647-652(1987).
CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
-1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
KW Cleavage on pair of basic residues; Hormone; Multigene family.
FT NON_TER 1 1
FT NON_CONS 10 11
FT NON_CONS 45 46
FT PEPTIDE 46 73
FT PEPTIDE 60 73
FT DISULFID 62 73
SQ SEQUENCE 73 AA; 7989 MW; CCCBA6B30DCB29BB CRC64;

Query Match 77.6%; Score 45; DB 1; Length 73;
Best Local Similarity 88.9%; Pred. No. 0.079; 1; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 1; -

QY 3 DNLPERRK 11
Db 51 NNLPERRK 59

RESULT 4

TRC4_ECOLI STANDARD; PRT; 1061 AA.

ID TRC4_ECOLI STANDARD; PRT; 1061 AA.
AC P27189; P27184;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DNA primase trAC (EC 2.7.7.-) (Replication primase).
GN TRAC.
OS Escherichia coli.
RP Plasmid IncP-beta RP4.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-14 AND 316-333.
RC STRAIN=HB101;
RX MEDLINE=92297959; PubMed=1818755;
RA Miele L., Strack B., Kruft V., Lankka E.;
RT "Gene organization and nucleotide sequence of the primase region of IncP plasmids RP4 and R751.";
RL DNA Seq. 2:145-162(1991).
CC -1- FUNCTION: REQUIRED FOR AUTONOMOUS REPLICATION IN ESCHERICHIA COLI.
CC -1- TRANSFERRED INTO THE RECIPIENT CELL DURING BACTERIAL CONJUGATION.
CC -1- CATALYZES THE SYNTHESIS OF SHORT OLIGORIBONUCLEOTIDE PRIMERS WITH
CC CPA. OR PCPA. AT THEIR 5'-TERMINI ON A SINGLE STRANDED
CC TEMPLATE DNA.
CC -1- ALTERNATIVE PRODUCTS: THE TRAC-1 AND TRAC-2 PROTEINS ARE PRODUCED.
CC -1- BY THE USE OF ALTERNATIVE INITIATION SITES.
CC -1- SIMILARITY: TO PLASMID R751 TRAC.
CC

QY 3 DNLPERRK 11
Db 51 NNLPERRK 59

RESULT 3

SMS2_ONCMY STANDARD; PRT; 115 AA.

ID SMS2_ONCMY STANDARD; PRT; 115 AA.

AC Q91194;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-Oct-2001 (Rel. 40, Last sequence update)
DT 16-Oct-2001 (Rel. 40, Last annotation update)
DE Somatostatin II precursor [Contains: [Tyr21,Gly24]somatostatin-28;
[Tyr7,Gly10]somatostatin-14].
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei.
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;

[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=95354921; PubMed=7628684;
RX MOORE C.A., Kittlison J.D., Dahl S.K., Sheridan M.A.;
RT "Isolation and characterization of a cDNA encoding for preprosomatostatin containing [Tyr7, Gly10]-somatostatin-14 from the endocrine pancreas of rainbow trout, Oncorhynchus mykiss.";
RT Gen. Comp. Endocrinol. 98:253-261(1995).
RL CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
CC
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CC
DR EMBL; U32471; AAC59695.1;
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin.
DR SIGNAL 1 18
RW Cleavage on pair of basic residues; Hormone; Signal; Multigene family.
FT PROTEIN 1 18
FT PEPTIDE 19 87
FT PEPTIDE 88 115
FT PEPTIDE 102 115
FT DISULFID 104 115
FT SEQUENCE 115 AA; 520595025FC6D91 CRC64;
SQ Query Match 77.6%; Score 45; DB 1; Length 115;
Best Local Similarity 88.9%; Pred. No. 0.13; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 8; -

QY 3 DNLPERRK 11
Db 93 NNLPERRK 101

RESULT 4

TRC4_ECOLI STANDARD; PRT; 1061 AA.

ID TRC4_ECOLI STANDARD; PRT; 1061 AA.
AC P27189; P27184;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DNA primase trAC (EC 2.7.7.-) (Replication primase).
GN TRAC.
OS Escherichia coli.
RP Plasmid IncP-beta RP4.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-14 AND 316-333.
RC STRAIN=HB101;
RX MEDLINE=92297959; PubMed=1818755;
RA Miele L., Strack B., Kruft V., Lankka E.;
RT "Gene organization and nucleotide sequence of the primase region of IncP plasmids RP4 and R751.";
RL DNA Seq. 2:145-162(1991).
CC -1- FUNCTION: REQUIRED FOR AUTONOMOUS REPLICATION IN ESCHERICHIA COLI.
CC -1- TRANSFERRED INTO THE RECIPIENT CELL DURING BACTERIAL CONJUGATION.
CC -1- CATALYZES THE SYNTHESIS OF SHORT OLIGORIBONUCLEOTIDE PRIMERS WITH
CC CPA. OR PCPA. AT THEIR 5'-TERMINI ON A SINGLE STRANDED
CC TEMPLATE DNA.
CC -1- ALTERNATIVE PRODUCTS: THE TRAC-1 AND TRAC-2 PROTEINS ARE PRODUCED.
CC -1- BY THE USE OF ALTERNATIVE INITIATION SITES.
CC -1- SIMILARITY: TO PLASMID R751 TRAC.
CC
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CC
 EMBL; XAA42455.1; -
 DR EMBL; X59793; CAA42456.1; -
 DR PIR; S37667; S37667;
 InterPro; IPR002936; Toprim.
 Pfam; PF01751; Toprim; 1;
 SMART; SM00493; TOPRIM; 1.
 DNA replication; Transferease; DNA-directed RNA polymerase; Plasmid;
 Alternative initiation.
 CHAIN 1 1061 DNA PRIMASE, ISOFORM TRAC-1.
 CHAIN 316 1061 DNA PRIMASE, ISOFORM TRAC-2.
 FT INIT_MET 316 FOR ISOFORM TRAC-2.
 FT SEQUENCE 1061 AA; 116722 MW; ABC344D2811B9B31 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 1061;
 Best Local Similarity 70.0%; Pred. No. 15;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VDNLPPRKH 11
 Db 140 IDGLPPLERK 149
 RESULT 5
 YFMT_THETH STANDARD; PRT; 110 AA.
 ID YFMT_THETH
 AC P43520;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical Protein in FMT 3' region (Fragment).
 OS Thermus aquaticus (subsp. thermophilus).
 OC Bacteria; Thermus/Deinococcus group; Thermus group; thermus.
 NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VK1;
 RX MEDLINE=95050326; PubMed=7961514;
 RA Meinel T.; Blanquet S.;
 RT "Characterization of the Thermus thermophilus locus encoding peptide
 deformylase and methionyl-tRNA(fmet) formyltransferase.";
 T J. Bacteriol. 176:7387-7390(1994).
 RL "SIMILARITY: BELONGS TO THE UPF0042 FAMILY.

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 or send an email to license@isb-sib.ch).
 CC
 DR HSSP; P19821; 1TAU.
 KW Hypothetical protein; ATP-binding.
 FT NP_BIND 8 15 ATP (POTENTIAL).
 FT NON_TER 110 110
 SQ SEQUENCE 110 AA; 12316 MW; C4F21341300F9DA6 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

RESULT 6
 SMS2_ORENI STANDARD; PRT; 28 AA.
 ID SMS2_ORENI
 AC P81029;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Somatostatin II Precursor [Contains: [Tyr21, Gly24] somatostatin-28];
 DE [Tyr7, Gly10] somatostatin-14 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Actinopterygii; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Acanthomorpha; Acanthopterygii; Teleostei; Neoteleostei;
 OC Cichlidae; Oreoichromis.
 NCBI_TaxID=8128;

RP SEQUENCE.
 RX MEDLINE=95384941; PubMed=7656183;
 RA Nguyen T.M.; Wright J.R. Jr.; Nielsen P.F.; Conlon J.M.;
 RT "Characterization of the pancreatic hormones from the Brockmann body
 of the tilapia: implications for islet xenograft studies.";
 RL Comp. Biochem. Physiol. 111C:33-44 (1995).
 CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin.
 KW Cleavage on pair of basic residues; Hormone; Multigene family.
 FT NON_TER 1 1
 FT PEPTIDE 1 28 [Tyr21, GLY24] SOMATOSTATIN-28.
 FT PEPTIDE 15 28 [Tyr7, GLY10] SOMATOSTATIN-14.
 FT DISULFID 17 28
 SQ SEQUENCE 28 AA; 3155 MW; 47C049F4866EF4AC CRC64;

Query Match 65.5%; Score 38; DB 1; Length 28;
 Best Local Similarity 66.7%; Pred. No. 0.51;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DNLPPRKR 11
 Db 6 NSLIPPRKR 14

RESULT 7
 S1FA_ARATH STANDARD; PRT; 76 AA.
 ID S1FA_ARATH
 AC P42551;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE DNA binding protein S1FA.
 GN S1FA.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicae; Arabidopsis; Arabidopsis.
 NCBI_TaxID=3702;

RP SEQUENCE FROM N.A.
 RC STRAIN=CV_COLUMBIA;
 RX MEDLINE=95148729; PubMed=7846151;
 RA Newman T.; de Brujin F.J.; Green P.; Keegstra K.; Kende H.;
 RA McIntosh L.; Ohlrogge J.B.; Raikhel N.; Somerville S.; Thomashow M.F.;
 RA Retzel E.; Somerville C.R.;
 RT "Genes Galore: a summary of methods for accessing results from large-
 scale partial sequencing of anonymous Arabidopsis cDNA clones.";
 RT Plant Physiol. 106:1241-1255 (1994).
 CC -1- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY RECOGNIZES A
 CC NEGATIVE ELEMENT (S1F) WITHIN THE RPS1 PROMOTER (BY SIMILARITY).

Qy 2 VDNLPPR 8
 11111111

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable)
 CC -1- SIMILARITY: STRONG, TO S1FA IN OTHER PLANTS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; T20524;
 KW NOT_ANNOTATED_CDS;
 SQ SEQUENCE 76 AA; 8252 MW; F05E3D5950F8A8AF CRC64;

Query Match 63.8%; Score 37; DB 1; Length 76;
 Best Local Similarity 75.0%; Pred. No. 2.5;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 DNLLPPRERK 11
 Db 48 NLPPRKKK 55

RESULT 8
 Y321_HAEIN HAEIN STANDARD PRT: 78 AA.
 ID Q57534;
 AC DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein HI0321.
 GN HI0321.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN SEQUENCE FROM N.A.
 RP STRAIN=RD / KW20 / ATCC 51907;
 RC RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedbloom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd";
 RN SEQUENCE FROM N.A.
 RP IDENTIFICATION BY MASS SPECTROMETRY.
 RX MEDLINE=20137488; PubMed=10675023;
 RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
 RA Gray C., Fountoulakis M.;
 RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
 RL Electrophoresis 21:411-429(2000).
 CC -1- SIMILARITY: SOME, TO B.NODOSUS.VIRULENCE-ASSOCIATED PROTEIN B
 (VAPB).

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 CC DR EMBL; U32717; AAC21984.1;

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 CC DR EMBL; U32717; AAC21984.1;

DR TIGR; HI0321;
 KW Complete proteome.
 SQ SEQUENCE 78 AA; 9037 MW; 468D048ED7C5C720 CRC64;
 Query Match 63.8%; Score 37; DB 1; Length 78;
 Best Local Similarity 66.7%; Pred. No. 2.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 DNLLPPRERK 11
 Db 68 DDLLPPQERE 76
 RESULT 9
 Y321_HAEIN HAEIN STANDARD PRT: 124 AA.
 ID Y321_HAEIN HAEIN STANDARD PRT: 124 AA.
 AC 054625;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 13.6 kDa protein STH24_04.
 GN STH24_04.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
 OC Streptomyces; Streptomycetaceae; Streptomyces.
 OC Actionomycetales; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=A3(2) / M145;
 RC RX MEDLINE=99014240; PubMed=9795152;
 RA Gal-Mor O., Borovok I., Av-Gay Y., Cohen G., Aharonowitz Y.;
 RT "Gene organization in the trxA/B-oriC region of the Streptomyces
 coelicolor chromosome and comparison with other eubacteria.";
 RT Gene 217:83-90(1998).
 RL [2] SEQUENCE FROM N.A.
 RP STRAIN=A3(2);
 RA Kim H.-D., Calcutt M.J., Schmidt F.J., Chater K.F.;
 RT "Partitioning of the linear chromosome during sporulation of
 Streptomyces coelicolor A3(2) involves an oriC-linked parAB locus.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3] SEQUENCE FROM N.A.
 RP STRAIN=A3(2);
 RC Oliver K., Harris D., James K.D., Parkhill J., Barrell B.G.,
 RA Rajandream M.A.;
 RA Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 CC [1- SIMILARITY: BELONGS TO THE UPF0161 FAMILY.
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 CC DR EMBL; Y16311; CAA76173.1;
 DR EMBL; AL049826; CAB42698.1;
 DR EMBL; AF187159; AAF16009.1;
 DR EMBL; AF031590; AAC03488.1;
 DR InterPro: IPR002696; DUF37.
 DR Pfam; PF01809; DUF37; 1;
 DR ProdDom; PD004225; DUF37; 1;
 KW HYPOTHETICAL PROTEIN;
 SQ SEQUENCE 124 AA; 13599 MW; 8BB3AD1786D8075E CRC64;

OC Schizosaccharomyctales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces;
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RI Lyne M., Rajandream M.A., Barrell B.G., Churcher C.M.,
 AC Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 CC -1- MISCELLANEOUS: THERE ARE THREE GENES FOR L7 IN S.POMBE.
 CC -1- SIMILARITY: BELONGS TO THE L30P FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 CC
 CC EMBL; AL022304; CAA18409.1;
 DR InterPro; IPR000517; Ribosomal_L30.
 DR Pfam; PF00327; Ribosomal_L30; 1.
 DR PROSITE; PS00634; RIBOSOMAL_L30; 1.
 KW Ribosomal protein; Multigene family.
 SQ SEQUENCE 251 AA; 28730 MW; 5382A27E39F3800E CRC64;
 [2]
 RN 63.8%; Score 37; DB 1; Length 251;
 RC Best Local Similarity 50.0%; Pred. No. 10;
 AC Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 DR Query Match 2 VDNLPPRERK 11
 DR :1:1:1:1:1
 DB 100 INNIPPKARK 109
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Oliver K., Harris D., Wood V., Barrell B.G., Rajandream M.A.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 CC -1- MISCELLANEOUS: THERE ARE THREE GENES FOR L7 IN S.POMBE.
 CC -1- SIMILARITY: BELONGS TO THE L30P FAMILY OF RIBOSOMAL PROTEINS.
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 CC
 DR EMBL; X54983; CAA38729.1; -;
 DR EMBL; 299296; CAB16592.1; -;
 DR PIR; S25067; S25067;
 DR InterPro; IPR000517; Ribosomal_L30.
 DR Pfam; PF00327; Ribosomal_L30; 1.
 DR PROSITE; PS00634; RIBOSOMAL_L30; 1.
 KW Ribosomal protein; Multigene family.
 SQ SEQUENCE 250 AA; 28449 MW; 2AE917F0DAF7A8CB CRC64;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Hart D.H., Gwynn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pampille W., Crosby M., Shen M.,
 RA Yamateyan J.J., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Mintz K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.,
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 CC -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) - AMP +
 CC diphosphate + L-phenylalanyl-tRNA(Phe).
 CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
 CC -1- SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -1- PHE-tRNA SYNTHETASE ALPHA CHAIN SUBFAMILY 1.
 CC
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 CC
 CC EMBL; AL022304; CAA18409.1;
 DR InterPro; IPR000517; Ribosomal_L30.
 DR Pfam; PF00327; Ribosomal_L30; 1.
 DR PROSITE; PS00634; RIBOSOMAL_L30; 1.
 KW Ribosomal protein; Multigene family.
 SQ SEQUENCE 251 AA; 28730 MW; 5382A27E39F3800E CRC64;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Oliver K., Rajandream M.A., Barrell B.G., Churcher C.M.,
 AC Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 CC -1- MISCELLANEOUS: THERE ARE THREE GENES FOR L7 IN S.POMBE.
 CC -1- SIMILARITY: BELONGS TO THE L30P FAMILY OF RIBOSOMAL PROTEINS.
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DR EMBL; AEE02066; AAF11900_1;
 DR HSSP; P27001; 1PYS.
 DR TIGR; DR2354;
 DR InterPro; IPR002106; AA_trNA_ligase_II.
 DR InterPro; IPR004188; Phe_trNA-synt_N.
 DR InterPro; IPR002319; tRNA-synt_2d.
 DR Pfam; PF02912; Phe_trNA-synt_N_1.
 DR Pfam; PF01409; tRNA-synt_2d_1.
 DR PROSITE; PS00179; AA_trNA_ligase_II_1;
 DR PROSITE; PS00339; AA_trNA_ligase_II_2;
 KW Aminocyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 Complete proteome.
 SQ SEQUENCE . 339 AA; 37549 MW; FA02BCD1C83A5BB5 CRC64;
 Query Match 63.8%; Score 37; DB 1; Length 339;
 Best Local Similarity 63.6%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 SVNDNLPPRERK 11
 Db 38 SLGKLPPEERK 48
 RESULT 13
 PSGA_HUMAN STANDARD PRT; 424 AA.
 ID Q15235;
 AC DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update).
 DE Pregnancy-specific beta-1-glycoprotein 10 precursor (PSBG-10).
 GN PSG10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=96006;
 RN 1
 RP SEQUENCE FROM N.A.
 RX TISSUE=Bone marrow;
 RC MEDLINE=91104939; PubMed=2271648;
 RA Barnett T.R., Pickle W. II, Elting J.J.;
 RA "Characterization of two new members of the pregnancy-specific beta 1-glycoprotein family from the myeloid cell line KG-1 and suggestion of two distinct classes of transcription unit.";
 RL Biochemistry 29:10213-10218 (1990).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- DEVELOPMENTAL STAGE: PSBG ARE PRODUCED IN HIGH QUANTITY DURING PREGNANCY.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CEA
 CC -1- SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC DR EMBL; X17098; CAA34957_1;
 CC DR InterPro; IPR003006; Ig_MHC.
 CC DR InterPro; IPR003598; Ig_c2;
 CC DR InterPro; IPR003600; Ig_like;
 CC Pfam; PF00047; Ig; 4.
 DR SMART; SM00410; Ig_like; 3.
 DR SMART; SM00408; IgC2; 1.
 KW Immunoglobulin domain; Glycoprotein; Signal; Repeat; Multigene family.
 FT SIGNAL 1 34
 CC BY SIMILARITY.
 CC PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 10.
 FT DOMAIN 35 143
 FT DOMAIN 161 223
 FT DOMAIN 254 316
 FT DOMAIN 346 400
 FT SITE 126 128
 FT DISULFID 168 216
 FT DISULFID 261 309
 FT DISULFID 353 393
 FT CARBOHYD 61 61
 FT CARBOHYD 103 103
 FT CARBOHYD 110 110
 FT CARBOHYD 198 198
 FT CARBOHYD 267 267
 FT CARBOHYD 302 302
 FT CARBOHYD 386 386
 FT CARBOHYD 419 419
 SQ SEQUENCE 424 AA; 47676 MW; OB726090B31B92E CRC64;
 Query Match 63.8%; Score 37; DB 1; Length 424;
 Best Local Similarity 54.5%; Pred. No. 18;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 SVNDNLPPRERK 11
 Db 244 TINNLNPREKK 254
 RESULT 14
 PSGC_HUMAN STANDARD PRT; 424 AA.
 ID Q75244;
 AC DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Pregnancy-specific beta-1-glycoprotein 12 precursor (PSBG-12).
 GN PSG12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=96006;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
 RA Burkhardt-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Barnes J.,
 RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
 RA Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G.,
 RA Coeffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
 RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
 RA Kobayashi A., Olsen A.S., Carrano A.V.;
 RA Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- DEVELOPMENTAL STAGE: PSBG ARE PRODUCED IN HIGH QUANTITY DURING PREGNANCY.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CEA
 CC -1- SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC DR EMBL; X17098; CAA34957_1;
 CC DR InterPro; IPR003006; Ig_MHC.
 CC DR InterPro; IPR003598; Ig_c2;
 CC DR InterPro; IPR003600; Ig_like;
 CC Pfam; PF00047; Ig; 4.

CC EMBL; AAC005260; Score 37; DB 1; Length 424;
 DR MIM; 176399; DR InterPro; IPB003006; DR InterPro; IPR003598; DR InterPro; IPR003600; DR Pfam; PF00047; SMART; SM00410; SMART; SM00408; FT SIGNAL 1 34 PROBABLE.
 FT DOMAIN 35 143 PROBABLE.
 FT DOMAIN 161 223 PROBABLE.
 FT DOMAIN 254 316 PROBABLE.
 FT DOMAIN 346 400 PROBABLE.
 FT SITE 126 128 PROBABLE.
 FT DISULFID 168 216 PROBABLE.
 FT DISULFID 261 309 PROBABLE.
 FT CARBOHYD 61 61 PROBABLE.
 FT CARBOHYD 103 103 PROBABLE.
 FT CARBOHYD 110 110 PROBABLE.
 FT CARBOHYD 198 198 PROBABLE.
 FT CARBOHYD 267 267 PROBABLE.
 FT CARBOHYD 302 302 PROBABLE.
 FT CARBOHYD 386 386 PROBABLE.
 FT CARBOHYD 419 419 PROBABLE.
 SQ SEQUENCE 424 AA; 47501 MW; 6ECB345E53CCDEA4 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 424;
 Best Local Similarity 54.5%; Pred. No. 18;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 SYVDNLPRERK 11
 Db 244 TINNLNFREKK 254

RESULT 15
 ID PSG6_HUMAN STANDARD: PRT; 435 AA.
 AC Q00889;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Pregnancy-specific beta-1-glycoprotein 6 precursor (PSBG-6).
 GN PSG6 OR CGM3 OR PSGGB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBITAXID=9606;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89392023; PubMed=2783133;

RA Zimmermann W., Weiss M., Thompson J.A.;
 RT "cDNA cloning demonstrates the expression of pregnancy-specific
 glycoprotein genes, a subgroup of the carinoembryonic antigen gene
 family, in fetal liver.";
 RT Biochem. Biophys. Res. Commun. 163:1197-1209 (1989).
 RN [2] SEQUENCE FROM N.A.
 RX MEDLINE=90211271; PubMed=1690992;
 RA Thommari R., Wagner K., Barnert S., Schleussner C.,
 Schrewe H., Zimmermann W., Mueller G., Schimpf W., Zaninetta D.,
 Ammastro D., Hardman N.;

RA "The human pregnancy-specific glycoprotein genes are tightly linked on
 the long arm of chromosome 19 and are coordinately expressed.";
 RT Biochem. Biophys. Res. Commun. 167:848-859 (1990).
 RN [3]

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FT	VARIANT	165	165	/FTId=VAR_011723.
FT	VARIANT	167	167	R -> L (IN DBSNP:1058680).
FT	VARIANT	180	180	/FTId=VAR_011724.
FT	VARIANT	181	181	I -> T (IN DBSNP:1065505).
FT	VARIANT	185	185	/FTId=VAR_011725.
FT	VARIANT	191	191	L -> W (IN DBSNP:1065507).
FT	VARIANT	196	196	/FTId=VAR_011726.
FT	VARIANT	253	253	L -> M (IN DBSNP:1065508).
FT	VARIANT	257	257	/FTId=VAR_011727.
FT	VARIANT	258	258	N -> S (IN DBSNP:1065509).
FT	VARIANT	344	344	/FTId=VAR_011728.
FT	VARIANT	404	404	R -> S (IN DBSNP:1058688).
FT	VARIANT	435	AA;	/FTId=VAR_011729.
SQ	SEQUENCE	48813	MW;	K -> E (IN DBSNP:1065511).
				/FTId=VAR_011730.
				K -> N (IN DBSNP:1065513).
				/FTId=VAR_011731.
				L -> S (IN DBSNP:1058710).
				/FTId=VAR_011732.
				A -> T (IN DBSNP:1065515).
				/FTId=VAR_011733.
				R -> H (IN DBSNP:1065519).
				/FTId=VAR_011734.
				I -> S (IN DBSNP:1065525).
				/FTId=VAR_011735.

Query Match 63.8%; Score 37; DB 1; Length 435;
 Best Local Similarity 54.5%; Pred. No. 19;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVDNLPPRERK 11
 Db 244 TINNLNPREKK 254

Search completed: June 13, 2002, 12:29:54
 Job time: 446 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 13, 2002, 12:22:56 ; Search time. 28.68 Seconds
(without alignments)
9.368 Million cell updates/sec

Title: US-09-727-739B-18
Perfect score: 58
Sequence: 1 SVDNLPPRERK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000.

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	67.2	219	4 US-09-247-373B-52	Sequence 52, Appl
2	39	67.2	224	4 US-09-247-373B-34	Sequence 34, Appl
3	37	63.8	424	6 5169835-6	Patent No. 5169835
4	36	62.1	2496	4 US-09-125-028-2	Sequence 2, Appl
5	36	62.1	2958	4 US-08-894-344C-2	Sequence 2, Appl
6	35	60.3	230	6 5169835-13	Patent No. 5169835
7	35	60.3	419	6 5169835-2	Sequence 2, Appl
8	35	60.3	591	3 US-09-082-737-2	Sequence 2, Appl
9	34	58.6	223	3 US-08-857-534-12	Sequence 12, Appl
10	34	58.6	223	5 PCT-US95-04971-12	Sequence 12, Appl
11	34	58.6	229	4 US-09-247-373B-48	Sequence 48, Appl
12	34	58.6	361	1 US-08-258-261B-3	Sequence 3, Appl
13	34	58.6	361	1 US-08-456-837-3	Sequence 3, Appl
14	34	58.6	361	1 US-08-457-342-3	Sequence 3, Appl
15	34	58.6	361	1 US-08-457-646A-3	Sequence 1, Appl
16	34	58.6	361	1 US-08-458-076A-3	Sequence 3, Appl
17	34	58.6	361	1 US-08-457-335A-3	Sequence 3, Appl
18	34	58.6	361	2 US-08-729-214-3	Sequence 3, Appl
19	34	58.6	361	3 US-09-028-934-3	Sequence 3, Appl
20	33	56.9	265	2 US-08-970-133-1	Sequence 1, Appl
21	33	56.9	265	4 US-09-294-545-1	Sequence 1, Appl
22	33	56.9	345	1 US-08-031-148-4	Sequence 4, Appl
23	33	56.9	345	3 US-08-415-838-4	Sequence 4, Appl
24	33	56.9	415	2 US-08-576-626A-52	Sequence 52, Appl
25	33	56.9	683	1 US-07-878-960-2	Sequence 2, Appl
26	33	56.9	855	1 US-08-344-536-2	Sequence 2, Appl
27	33	56.9	855	1 US-08-344-536-1	Sequence 5, Appl

Sequence 2, Appl
Sequence 5, Appl
Sequence 32, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 30, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 44, 3 US-08-920-562-2
Sequence 5, 3 US-08-920-562-5
Sequence 2544, 2 US-08-576-626A-32
Sequence 275, 4 US-09-147-915-4
Sequence 296, 3 US-08-986-769-2
Sequence 361, 3 US-09-028-934-30
Sequence 449, 1 US-08-624-663A-2
Sequence 449, 2 US-08-974-565C-1
Sequence 449, 3 US-09-255-748-1
Sequence 470, 4 US-09-004-838-44
Sequence 472, 4 US-09-004-838-43
Sequence 560, 3 US-08-648-650A-2
Sequence 560, 3 US-08-648-650A-2
Sequence 600, 3 US-08-904-871-3
Sequence 713, 2 US-08-987-466-3
Sequence 713, 2 US-08-974-565C-5
Sequence 713, 3 US-09-255-748-5
Sequence 713, 4 US-09-240-359-3

ALIGMENTS

RESULT 1
US-09-247-373B-52
; Sequence 52, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; INVENTOR: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1108-A
; CURRENT APPLICATION NUMBER: US/09/247-373B
; CURRENT FILING DATE: 1999-02-10
; PRIORITY APPLICATION NUMBER: 08/924,747
; PRIORITY FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 52
; LENGTH: 219
; TYPE: PRT
; ORGANISM: SOYBEAN
US-09-247-373B-52

RESULT 2
US-09-247-373B-34
; Sequence 34, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; INVENTOR: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1108-A
; CURRENT APPLICATION NUMBER: US/09/247-373B
; CURRENT FILING DATE: 1999-02-10
; PRIORITY APPLICATION NUMBER: 08/924,747
; PRIORITY FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 34
; LENGTH: 224
; TYPE: PRT
; ORGANISM: SOYBEAN

US-09-247-373B-34

Query Match 67.2%; Score 39; DB 4; Length 224;
 Best Local Similarity 75.0%; Pred. No. 8.7;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DNLPFR 10
 Db 202 DNLPFRDK 209

RESULT 3

5169835-6
 Patent No. 5169835
 Applicant: WAI-YEE, CHAN
 Title of Invention: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
 Number of Sequences: 48
 Current Application Data:
 Application Number: US/07/390,409
 Filing Date: 07-AUG-1989
 SEQ ID NO:6:
 LENGTH: 424

Query Match 63.8%; Score 37; DB 6; Length 424;
 Best Local Similarity 54.5%; Pred. No. 39;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVDNLPPRER 11
 Db 244 TINNLNPREKK 254

RESULT 4

US-09-125-028-2
 Sequence 2, Application US/09125028A
 Patent No. 61907 07
 General Information:
 Applicant: WADOUX, Isabelle
 Applicant: COLAVIZZA, Didier
 Applicant: LOIEZ, Annie
 Title of Invention: NOVEL COLD-SENSITIVE BREAD-MAKING YEASTS.
 File Reference: levure sensible froid
 Current Application Number: US/09/125,028A
 Current Filing Date: 1998-08-07
 Earlier Application Number: PCT/FR97/00254
 Number of SEQ ID NOS: 2
 Software: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 2496
 Type: PRT
 Organism: Saccharomyces cerevisiae
 US-09-125-028-2

APPLICANT: TOKAI, Masaya

APPLICANT: KIKUCHI, Yasuhiro

APPLICANT: OUCHI, Kozo

TITLE OF INVENTION: DNA ENCODING PROTEIN COMPLEMENTING

TITLE OF INVENTION: YEAST

TITLE OF INVENTION: LOW TEMPERATURE-SENSITIVE FERMENTABILITY

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10112-3801

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.50 inch, 1440 Kb storage.

COMPUTER: IBM PS/V

OPERATING SYSTEM: MS-DOS Ver3.30

SOFTWARE: PATENT AID Ver1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,344C

FILING DATE: 15-AUGUST-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP343700/95

FILING DATE: 28-DECEMBER-1995

APPLICATION NUMBER: PCT/JP96/03862

FILING DATE: 27-DECEMBER-1996

ATTORNEY/AGENT INFORMATION:

NAME: Perry, Lawrence S.

REGISTRATION NUMBER: 31865

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-218-2100

TELEFAX: 212-218-2200

INFORMATION FOR SEQ ID NO: 2

SEQUENCE CHARACTERISTICS:

LENGTH: 2958 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Saccharomyces cerevisiae

STRAIN: X2180-1B

US-08-894-344C-2

Query Match 62.1%; Score 36; DB 4; Length 2958;

Best Local Similarity 66.7%; Pred. No. 4.6e+02;

Matches 6; Conservative 1; Indels 0; Gaps 0;

Qy 2 VDNLPPRER 10
 Db 257 IDVLPPKER 265

RESULT 6

5169835-13

; Patent No. 5169835

; APPLICANT: WAI-YEE, CHAN

; TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS

; NUMBER OF SEQUENCES: 48

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/390,409

; FILING DATE: 07-AUG-1989

; SEQ ID NO:13:

; LENGTH: 230

; 5169835-13

RESULT 5
 US-08-894-344C-2
 Sequence 2, Application US/08894344C
 Patent No. 6172196
 General Information:
 Applicant: KAWASAKI, Hideki

Query Match 60.3%; Score 35; DB 6; Length 230;

Best Local Similarity 54.5%; Pred. No. 4.6;

Matches 3; Conservative 2; Indels 2; Gaps 0;

Qy 2 VDNLPPRER 10
 Db 257 IDVLPPKER 265

Query Match 1 SYDNLPPRER 11

RESULT 7
 5169835-2
 ; Patent No. 5169835
 ; APPLICANT: WAI-YEE, CHAN
 ; TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
 ; NUMBER OF SEQUENCES: 48
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/390,409
 ; FILING DATE: 07-AUG-1989
 ; SEQ ID NO:2;
 ; LENGTH: 419
 5169835-2

Query Match 60.3%; Score 35; DB 6; Length 419;
 Best Local Similarity 54.5%; Pred. No. 88;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 SVDNLPPRERK 11
 Db 245 TINNLNPRENK 255

RESULT 8
 US-09-082-737-2
 ; Sequence 2, Application US/09082737
 ; Patent No. 6013500
 ; GENERAL INFORMATION:
 ; APPLICANT: Minden, Audrey
 ; TITLE OF INVENTION: PAK4; A No. 6013500el Gene Encoding A Serine/
 ; TITLE OF INVENTION: Threonine Kinase
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Durham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 11230

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/082,737
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0575/553311
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 591 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-09-082-737-2

Query Match 58.6%; Score 34; DB 3; Length 223;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPRERK 11
 Db 44 PPRERK 49

RESULT 10
 PCT-US95-04971-12
 ; Sequence 12, Application PC/TUS9504971
 ; GENERAL INFORMATION:
 ; APPLICANT: George W. Kemble
 ; TITLE OF INVENTION: A Novel VZV Gene, Mutant VZV and Immunogenic
 ; TITLE OF INVENTION: Compositions
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 ; STREET: 5 Palo Alto Square
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306

Query Match 60.3%; Score 35; DB 3; Length 591;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 DNLPPR 8

Db 529 DNLPPR 534

RESULT 9
 US-08-857-534-12
 ; Sequence 12, Application US/08857534
 ; Patent No. 6087170
 ; GENERAL INFORMATION:
 ; APPLICANT: George W. Kemble
 ; TITLE OF INVENTION: A No. 6087170el VZV Gene, Mutant VZV and Immunogenic
 ; TITLE OF INVENTION: Compositions
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 ; STREET: 5 Palo Alto Square
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306

Query Match 58.6%; Score 34; DB 3; Length 223;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPRERK 11
 Db 44 PPRERK 49

RESULT 10
 PCT-US95-04971-12
 ; Sequence 12, Application PC/TUS9504971
 ; GENERAL INFORMATION:
 ; APPLICANT: George W. Kemble
 ; TITLE OF INVENTION: A Novel VZV Gene, Mutant VZV and Immunogenic
 ; TITLE OF INVENTION: Compositions
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 ; STREET: 5 Palo Alto Square
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04971
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/235,406
 FILING DATE: APRIL 28, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Luann Cerr
 REGISTRATION NUMBER: 31,822
 REFERENCE/DOCKET NUMBER: AVIR-004/00WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5165
 TELEFAX: 415-857-0663
 TELEX: 380816 COOLEYPA
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 223 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: Protein
 PCT-0095-04971-12

Query Match 58.6%; Score 34; DB 5; Length 223;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPRERK 11
 Db 44 PPRERK 49

RESULT 11
 US-09-247-373B-48
 Sequence 48, Application US/09247373B
 Patent No. 6168954
 GENERAL INFORMATION:
 APPLICANT: McGONIGLE, BRIAN
 APPLICANT: O'KEEFE, DANIEL
 TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
 FILE REFERENCE: CL-1108-A

CURRENT APPLICATION NUMBER: US/09/247,373B
 CURRENT FILING DATE: 1999-02-10
 PRIOR APPLICATION NUMBER: 08/924,747
 PRIOR FILING DATE: 1997-09-05
 NUMBER OF SEQ ID NOS: 56
 SEQ ID NO 48
 LENGTH: 229
 TYPE: PRT
 ORGANISM: SOYBEAN

US-09-247-373B-48
 Sequence 34, DB 4; Length 229;
 Best Local Similarity 62.5%; Pred. No. 70;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 DNLPFR 10
 Db 200 DSLPPRDK 207

RESULT 12
 US-08-258-261B-3
 Sequence 3, Application US/08258261B
 Patent No. 5639949
 Sequence 3, Application US/08456837
 Patent No. 5643774

GENERAL INFORMATION:
 APPLICANT: Schupp, Thomas
 APPLICANT: Ligon, James M.
 APPLICANT: Beck, James Joseph
 APPLICANT: Hill, Dwight Steven
 APPLICANT: Ryals, John Andrew
 APPLICANT: Gaffney, Thomas Deane
 APPLICANT: Lam, Stephen Ting
 APPLICANT: Hammer, Phillip E.
 APPLICANT: Uknnes, Scott Joseph
 TITLE OF INVENTION: Genes for the synthesis of
 antipathogenic substances
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ciba-Geigy Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: NY
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/258,261B
 FILING DATE: 08-JUN-1994
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/457,205
 FILING DATE: 01-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8614
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 361 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-258-261B-3

Query Match 58.6%; Score 34; DB 1; Length 361;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NLPPRE 9
 Db 107 NLPPRE 112

RESULT 13

US-08-456-837-3
 Sequence 3, Application US/08456837
 Patent No. 5643774

GENERAL INFORMATION:
 APPLICANT: Schupp, Thomas
 APPLICANT: Ligon, James M.
 APPLICANT: Beck, James Joseph
 APPLICANT: Hill, Dwight Steven
 APPLICANT: Ryals, John Andrew
 APPLICANT: Gaffney, Thomas Deane
 APPLICANT: Lam, Stephen Ting
 APPLICANT: Hammer, Phillip E.
 APPLICANT: Uknnes, Scott Joseph
 TITLE OF INVENTION: Genes for the synthesis of
 antipathogenic substances
 NUMBER OF SEQUENCES: 22

NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ciba-Geigy Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: NY
 COUNTRY: USA
 ZIP: 10532

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/456, 837
 FILING DATE: 01-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/457, 205
 FILING DATE: 01-JUN-1995
 APPLICATION NUMBER: 08/258, 261
 FILING DATE: 08-Jun-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8614
 TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 361 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-456-837-3

Query Match 58.6%; Score 34; DB 1; Length 361;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 NLPPRE 9
 Db 107 NLPPRE 112

RESULT 15
 US-08-457-646A-3
 Sequence 3, Application US/08457646A
 Patent No. 5679560

GENERAL INFORMATION:
 APPLICANT: Schupp, Thomas
 APPLICANT: Ligon, James M.
 APPLICANT: Beck, James Joseph
 APPLICANT: Hill, Dwight Steven
 APPLICANT: Ryals, John Andrew
 APPLICANT: Gaffney, Thomas Deane
 APPLICANT: Lam, Stephen Ting
 APPLICANT: Hammer, Phillip E.

APPLICANT: Oknes, Scott Joseph
 TITLE OF INVENTION: Genes for the synthesis of
 antipathogenic substances
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ciba-Geigy Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: NY
 COUNTRY: USA
 ZIP: 10532

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/457, 646A
 FILING DATE: 01-JUN-1995
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/457, 205
 FILING DATE: 01-JUN-1995

APPLICANT: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

APPLICATION NUMBER: 08/258, 261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-457-646A-3

Query Match 58.6%; Score 34; DB 1; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 NLPPRE 9
| | | | |
Db 107 NLPPRE 112

Search completed: June 13, 2002, 12:22:56
Job time: 194 sec

FT Peptide 98..111 /note= "SS-14 variant peptide"

FT CA2325169-A1.

XX PN 03-JUN-2001.

PD 01-DEC-2000; 2000CA-2325169.

XX PF 03-DEC-1999; 99US-0168934.

XX PA (NDSU-) NDSU RES FOUND.

XX PI Sheridan MA, Moore CA, Kittelson JD; WPI; 2001-425997/46.

DR N-PSDB; AAS12935.

XX PT New somatostatin polypeptides derived from *Oncorhynchus mykiss*, useful for treating diabetes mellitus, acromegaly, gastrinoma, acquired immunodeficiency syndrome and neurological disorders -

X PS Claim 1; Fig 3; 52PP; English.

XX The invention relates to an *Oncorhynchus mykiss* somatostatin polypeptide containing a portion of preprosomatostatin I (PPSS-I) and/or a portion of preprosomatostatin II (PPSS-II). The protein sequences and their associated polynucleotides are useful for identifying modified somatostatin polypeptides which functions as a somatostatin agonist useful for research, therapeutics or diagnostics, including medical and veterinary applications. The wild-type somatostatin and its modified version are useful for treating hypersecretion from endocrine tumours in the pituitary (e.g. acromegaly) or gastrointestinal/pancreatic tissues (e.g. gastrinoma, glucagonoma, carcinoid syndrome), to cause tumour shrinkage through their effects on cell proliferation and apoptosis and as adjuncts in the treatment of diabetes mellitus via inhibition of growth hormone and glucagon. In addition, dysfunctional somatostatin secretion is associated with acquired immunodeficiency syndrome (AIDS) and various neurological disorders (e.g. epilepsy, Alzheimer's disease and Huntington's disease) and somatostatin antagonists are effective in the treatment of such conditions. Nucleic acids encoding the polypeptides are useful in gene therapy and fusion peptides can be targeted to neoplasms and their metastases, inhibiting the release of their secretory products. This sequence represents O. Mykiss PPSS-II', protein. Note: The features for this sequence are specifically claimed in the specification.

XX SQ Sequence 111 AA;

CC The invention relates to an *Oncorhynchus mykiss* somatostatin polypeptide containing a portion of preprosomatostatin I (PPSS-I) and/or a portion of preprosomatostatin II (PPSS-II). The protein sequences and their associated polynucleotides are useful for identifying modified somatostatin polypeptides which functions as a somatostatin agonist useful for research, therapeutics or diagnostics, including medical and veterinary applications. The wild-type somatostatin and its modified version are useful for treating hypersecretion from endocrine tumours in the pituitary (e.g. acromegaly) or gastrointestinal/pancreatic tissues (e.g. gastrinoma, glucagonoma, carcinoid syndrome), to cause tumour shrinkage through their effects on cell proliferation and apoptosis and as adjuncts in the treatment of diabetes mellitus via inhibition of growth hormone and glucagon. In addition, dysfunctional somatostatin secretion is associated with acquired immunodeficiency syndrome (AIDS) and various neurological disorders (e.g. epilepsy, Alzheimer's disease and Huntington's disease) and somatostatin antagonists are effective in the treatment of such conditions. Nucleic acids encoding the polypeptides are useful in gene therapy and fusion peptides can be targeted to neoplasms and their metastases, inhibiting the release of their secretory products. This sequence represents O. Mykiss PPSS-II', protein. Note: The features for this sequence are specifically claimed in the specification.

XX SQ Sequence 111 AA;

CC The invention relates to an *Oncorhynchus mykiss* somatostatin polypeptide containing a portion of preprosomatostatin I (PPSS-I) and/or a portion of preprosomatostatin II (PPSS-II). The protein sequences and their associated polynucleotides are useful for identifying modified somatostatin polypeptides which functions as a somatostatin agonist useful for research, therapeutics or diagnostics, including medical and veterinary applications. The wild-type somatostatin and its modified version are useful for treating hypersecretion from endocrine tumours in the pituitary (e.g. acromegaly) or gastrointestinal/pancreatic tissues (e.g. gastrinoma, glucagonoma, carcinoid syndrome), to cause tumour shrinkage through their effects on cell proliferation and apoptosis and as adjuncts in the treatment of diabetes mellitus via inhibition of growth hormone and glucagon. In addition, dysfunctional somatostatin secretion is associated with acquired immunodeficiency syndrome (AIDS) and various neurological disorders (e.g. epilepsy, Alzheimer's disease and Huntington's disease) and somatostatin antagonists are effective in the treatment of such conditions. Nucleic acids encoding the polypeptides are useful in gene therapy and fusion peptides can be targeted to neoplasms and their metastases, inhibiting the release of their secretory products. This sequence represents O. Mykiss PPSS-II', protein. Note: The features for this sequence are specifically claimed in the specification.

XX FT Key 23

FT Misc-difference /label= "Hyl, Lys"

XX PN EP173527-A.

XX PD 05-MAR-1986.

XX PF 16-AUG-1985; 85EP-0305867.

XX PR 31-AUG-1984; 84US-0646610.

XX PA (SALK) SALK INST FOR BIOL STUD.

XX PI Spiess J, Noe BD;

XX DR WPI; 1986-063363/10.

XX PT Angler fish somatostatin-28 and analogue and fragment - useful in inhibiting insulin secretion in insulinoma.

XX PS Claim 4; Page 18; 19pp; English.

XX CC The protein sequence is an insulin-selective analogue of anglerfish somatostatin-28, which is more potent than somatostatin-14 or somatostatin-28 in inhibiting insulin secretion for treatment of insulinoma.

XX SQ Sequence 28 AA;

Query Match 84.5%; Score 49; DB 7; Length 28;

Best Local Similarity 81.8%; Pred. No. 0.048;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 4 svdnlprrk 14

QY 1 SVDNLPPRERK 11

DB 4 :|||||||

RESULT 3

AAP90989

ID AAP90989 standard; peptide; 28 AA.

XX AC AAP90989;

XX DT 08-JUN-1990 (first entry)

XX DE Analogue of anglerfish somatostatin 28.

XX KW Somatostatin 28; SS-28; analogue; insulin secretion inhibitor; insulinoma; gastric acid secretion; thermoregulation.

XX OS Anglerfish.

XX FT Key 17

FT Disulfide-bond /note= "Bonded to Cys-28"

FT Disulfide-bond 28

FT Misc-difference 23

FT /label= "Lys, Hyl"

FT Region 15..28

FT /note= "Also claimed"

XX PN US4816438-A.

XX PD 28-MAR-1989.

XX AC AAP61714;

XX DT 28-JUL-1991 (first entry)

XX DE Somatostatin-28 analogue.

XX KW Somatostatin-28; insulin-selective; insulinoma.

OS Synthetic.

XX PR 01-APR-1987; 87US-0033295.

XX PR 01-APR-1987; 87US-0033295.

PR 31-AUG-1984; 84US-0646610.

XX (SALK) SALK INST FOR BIOL STUD.
 PA XX Spiess J, Noe BD;
 PI XX WPI; 1989-113910/15.
 PT XX Angler fish somatostatin-28 and fragments -
 PT useful in inhibiting insulin secretion and insulinoma
 PS XX Claim 1; page 65; 8pp; English.
 XX It is called ass-28 because it is an analogue of anglerfish somatostatin (SS-28). It is more potent than either somatostatin-14 (SS-14) or SS-28 at inhibiting insulin secretion for the treatment of insulinoma. The 14-residue C-terminal peptide is also claimed (ass-14). ass-14 is useful for inhibiting insulin secretion by the pancreas. ass-28 and ass-28 may be useful for decreasing gastric acid secretion and influencing thermoregulation. Their reduced linear forms, wherein the disulphide bridge is not present and is replaced by H, is also claimed.
 XX Sequence 28 AA;
 XX

Query Match 84.5%; Score 49; DB 10; Length 28;
 Best Local Similarity 81.8%; Pred. No. 0.048; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 SVDNLPPRERK 11
 Db 4 stnnlpprerk 14

RESULT 4
 AAP20029 AAP20029 standard; Protein; 125 AA.
 XX AC AAP20029;
 XX DT 14-AUG-1992 (first entry)
 XX DE Sequence of preprosomatostatin-2 encoded on pLAS2.
 XX KW Somatostatin; growth hormone; peptide hormone; secretion.
 XX FH Key Location/Qualifiers
 FT Protein 112..125
 FT /label= Somatostatin II
 XX PN EP46669-A.
 XX PD 03-MAR-1982.
 XX PF 21-AUG-1981; 81EP-0303825.
 XX PR 25-AUG-1980; 80US-0181046.

XX PA (REGC) UNIV OF CALIFORNIA:
 XX Hobart P, Crawford R, Pictet RL, Rutter WJ;
 XX WPI; 1982-18113E/10.
 XX DR N-PSDB; AAN20034.
 XX PT New somatostatin and precursors - produced by transformed
 PT microorganisms
 PS XX Example; Fig 3; 50pp; English.
 XX

CC The inventors claim preprosomatostatin-1, prosomatostatin-1,
 CC preprosomatostatin-2, somatostatin-2 and somatostatin-2; and DNA
 CC encoding them. The translation of somatostatin mRNA yields a
 CC precursor (prepro S1) containing a signal peptide which may be
 CC released during the transit into the endoplasmic reticulum, and the
 CC resultant precursor (pro S1) is subsequently cleaved to yield S1
 CC itself. The prepeptide portion of prepro S1 is probably about 20-25
 CC bases long. Translation of pLAS2 predicts the sequence of a 125 AA
 CC peptide which surprisingly contains a 14 AA sequence at its carboxy
 CC terminus which differs from S1 by only 2 AAs, and is termed
 CC Somatostatin 2. (S2).
 XX SQ Sequence 125 AA;

CC released during the transit into the endoplasmic reticulum, and the
 CC resultant precursor (pro S1) is subsequently cleaved to yield S1
 CC itself. The prepeptide portion of prepro S1 is probably about 20-25
 CC bases long. Translation of pLAS2 predicts the sequence of a 125 AA
 CC peptide which surprisingly contains a 14 AA sequence at its carboxy
 CC terminus which differs from S1 by only 2 AAs, and is termed
 CC Somatostatin 2. (S2).
 XX SQ Sequence 125 AA;

Query Match 84.5%; Score 49; DB 3; Length 125;
 Best Local Similarity 81.8%; Pred. No. 0.23;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 SVDNLPPRERK 11
 Db 101 stnnlpprerk 111

RESULT 5
 ABB62651 ABB62651 standard; Protein; 845 AA.

XX ID ABB62651; AC ABB62651;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 14745.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL06754.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX PS Disclosure; SEQ ID NO 14745; 21pp + Sequence Listing; English.
 XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL3011), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 845 AA;

Query Match 79.3%; Score 46; DB 22; Length 845;
 XX

Best Local Similarity 88.9%; Pred. No. 5.9;
Matches 8; Conservative 1; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 SVDNLLPPRE 9
ID AAU07667 standard; protein; 115 AA;
XX
Db 641 svdnippe 649

RESULT 6
AAU07667
ID AAU07667 standard; protein; 115 AA;
XX
AC AAU07667;
XX
DT 04-DEC-2001 (first entry)
XX
DE Rainbow trout preprosomatosatin II (PPSS-II') polypeptide.
XX
KW Rainbow trout; somatosatin; preprosomatosatin; hypersecretion; PPSS-I;
KW PPSS-II'; PPSS-II'; endocrine tumour; pituitary gland; glucagonoma; AIDS;
KW gastroenteropancreatic tissue; acromegaly; gastrinoma; diabetes mellitus;
KW carcinoid syndrome; cell proliferation; apoptosis; growth hormone;
W glucagon; acquired immunodeficiency syndrome; neurological disorder; HIV;
KW epilepsy; Alzheimer's disease; Huntington's disease; neuroprotective;
KW neoplasm; metastasis; gene therapy; antidiabetic; nootropic; cytostatic;
KW anti-human immunodeficiency virus; osteopathic; anticonvulsant.
XX
OS Oncorhynchus mykiss.

XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /note= "Signal peptide"
FT Protein 1..87
FT /note= "PPSS-II' pre-sequence"
FT Protein 26..115
FT /note= "Mature PPSS-II'"
FT Misc-difference 74
FT /note= "Encoded by CAA"
FT Peptide 88..101
FT /note= "PPSS-II' pro-sequence"
FT Peptide 88..115
FT /note= "Prosomatosatin II'"
FT Cleavage-site 100..101
FT /note= "Dibasic cleavage site"
FT Peptide 102..115
FT /note= "SS-14 variant peptide"
XX
PN CA2325169-A1.
XX
D 03-JUN-2001.
X
PF 01-DEC-2000; 2000CA-2325169.
XX
PR 03-DEC-1999; 99US-0168934.
XX
(NDSU-) NDSU RES FOUND.
XX
PI Sheridan MA, Moore CA, Kittelson JD;
XX
WPI: 2001-425997/46.
DR N-PSDB; AAS12934.
XX
PT New somatosatin polypeptides derived from *Oncorhynchus mykiss*, useful
PT for treating diabetes mellitus, acromegaly, gastrinoma, acquired
PT immunodeficiency syndrome and neurological disorders -
XX
PS Claim 2: Fig 3; 52pp; English.
XX
CC The invention relates to an *Oncorhynchus mykiss* somatosatin polypeptide
CC containing a portion of preprosomatosatin I (PPSS-I) and/or a portion of
CC preprosomatosatin II (PPSS-II). The protein sequences and their
CC associated polynucleotides are useful for identifying modified
CC somatosatin polypeptides which functions as a somatosatin agonist useful

CC for research, therapeutics or diagnostics, including medical and
CC veterinary applications. The wild-type somatosatin and its modified
CC version are useful for treating hypersecretion from endocrine tumours in
CC the pituitary (e.g. acromegaly) or gastronectropancreatic tissues (e.g.
CC gastrinoma, glucagonoma, carcinoid syndrome), to cause tumour shrinkage
CC through their effects on cell proliferation and apoptosis and as adjuncts
CC in the treatment of diabetes mellitus via inhibition of growth hormone
CC and glucagon. In addition, dysfunctional somatosatin secretion is
CC associated with acquired immunodeficiency syndrome (AIDS) and various
CC neurological disorders (e.g. epilepsy, Alzheimer's disease and
CC Huntington's disease) and somatosatin antagonists are effective in the
CC treatment of such conditions. Nucleic acids encoding the polypeptides are
CC useful in gene therapy and fusion peptides can be targeted to neoplasms
CC and their metastases, inhibiting the release of their secretory products.
CC This sequence represents O. Mykiss PPSS-II' protein.
CC Note: The features for this sequence are specifically claimed in the
CC specification.

XX
Sequence 115 AA;
Query Match 77.6%; Score 45; DB 22; Length 115;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DNLLPPRERK 11
Db 93 nnlppprerk 101.

RESULT 7
ID AAM38940 standard; Protein; 290 AA.
XX
AC AAM38940;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2085.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO2001153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR N-PSDB; AAI58096.

PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries
 XX Example 3; SEQ ID NO 2085; 10078pp; English.
 PS The invention relates to human nucleic acids (AAI57798-AAI61369) and
 XX the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as,
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S. disorders.
 Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX Sequence 290 AA;

Query Match 69.0%; Score 40; DB 22; Length 290;
 Best Local Similarity 72.7%; Pred. No. 24;
 Matches 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVVDNLPPRERK 11
 DB 193 swdslppserk 203

RESULT 8
 ABB63556 ID ABB63556 standard; Protein; 1006 AA.
 XX ABB63556;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 17460.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX JS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI: 2001-656860/75.
 XX N-PSDB; ABL07659.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 PS Disclosure; SEQ ID NO 17460; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1006 AA;

Query Match 69.0%; Score 40; DB 22; Length 1006;
 Best Local Similarity 60.0%; Pred. No. 87;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVVDNLPPRER 10
 DB 444 atdnmpkr 453

RESULT 9
 AAB07849 ID AAB07849 standard; Protein; 219 AA.
 XX AC AAB07849;
 XX DT 14-NOV-2000 (first entry)
 XX DE Amino acid sequence of a soybean type III glutathione-S-transferase.
 XX KW Soybean; glutathione-S-transferase; GST; detoxification;
 KW xenobiotic compound; herbicide-tolerance; transgenic plant;
 KW herbicide synergist.
 XX OS Glycine max.
 XX PN WO200047728-A2.
 XX PD 17-AUG-2000.
 XX PF 10-FEB-2000; 2000WO-US03347.
 XX PR 10-FEB-1999; 99US-0247373.
 XX PA (DUO) DÜ PONT DE NEMOURS & CO E I.
 XX PI McGonigle B, O'Keefe DP;
 XX DR N-PSDB; AAA59484.

XX The present sequence represents a soybean glutathione-S-transferase
 CC (GST) enzyme. The enzyme is involved in the detoxification of
 CC xenobiotic compounds in plants and seeds. The GST polynucleotides
 CC and polypeptides are used for the production of herbicide-tolerant
 CC transgenic plants, and for the development of screening assays to
 CC identify GST inhibitors and substrates, which can be used as
 CC herbicide synergists. GST Gene specific probes can be used in gene
 CC identification methods. The recombinant GST enzymes can be used to
 CC produce enzyme specific antibodies which are used to detect the
 CC enzymes in situ in cells or in vitro in cell extracts.
 XX Sequence 219 AA;

17-AUG-2000.
10-FEB-2000; 2000WO-US03347.
10-FEB-1999; 99US-0247373.
(DUPO) DU PONT DE NEMOURS & CO E I.
McGonigle B, O'Keefe DP;
WPI; 2000-549144/50.
N-PSDB; AAA59475.
Soybean glutathione-S-transferase polypeptides and polynucleotides used to produce herbicide tolerant transgenic plants and to screen for inhibitors or substrates of the enzyme
Claim 26; Page 71-72; 84pp; English.
The present sequence represents a soybean glutathione-S-transferase (GST) enzyme. The enzyme is involved in the detoxification of xenobiotic compounds in plants and seeds. The GST polynucleotides and polypeptides are used for the production of herbicide-tolerant transgenic plants, and for the development of screening assays to identify GST inhibitors and substrates, which can be used as herbicide synergists. GST Gene specific probes can be used in gene identification methods. The recombinant GST enzymes can be used to produce enzyme specific antibodies which are used to detect the enzymes *in situ* in cells or *in vitro* in cell extracts.

```
Query Match 67.28; score 39; DB 21; Length 224;
Best Local Similarity 75.08; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 11
AG82843
D : AG82843 standard; Protein: 244 AA.

11-FEB-2002 (first entry)
Probationary Police Recruit SPC ID NO 1844
ABD2920,

XX Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
 KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
 KW systemic infection; non-diarrhoeal infection; septicaemia;
 KW pyelonephritis; antibiotic resistance.
 XX Escherichia coli.
 OS
 PN WO200166572-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 12-MAR-2001; 2001WO-EP03445.
 XX PR 10-MAR-2000; 2000FR-0003145.
 XX PR 02-FEB-2001; 2001FR-0001449.
 XX PA (INRM) INSEMR INST NAT SANTE & RECH MEDICALE.
 XX
 I Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;
 DR 2001-550253/61.
 XX
 PT A library of DNA fragments of Escherichia coli strains for the
 PT phylogenetic determination of a given strain comprises polynucleotides of
 PT nature B2/D+ A- -
 XX
 PS Example 6; Fig 6; 646pp; English.
 XX The invention relates to a library of DNA fragments of Escherichia coli
 CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533)
 CC and encoded Proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of nature
 B2/D+A-. The polynucleotides have potential antiinflammatory,
 CC antibacterial and immunosuppressive activity as part of pharmaceutical
 CC compositions used to treat, palliate or prevent extra-intestinal E. coli
 CC infections. The polypeptides are useful for determining the phylogenetic
 CC group of a given E. coli strain. These polypeptides can detect and treat
 CC an undesired development of E. coli, particularly an extra-intestinal
 CC infection that include systemic and non-diarrhoeal infections such as
 CC septicaemia, pyelonephritis and meningitis this is particularly
 CC advantageous as bacterial resistance is increasing with the more
 CC frequent use of broad spectrum antibiotics
 XX
 SQ sequence 370 AA;

XX
 Query Match 67.2%; Score 39; DB 22; Length 370;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 2 VDNLPPR 8
 DE |||||
 DB 169 vdnlppr 175
 XX
 RESULT 13
 ID ABB69479 standard; Protein: 796 AA.
 XX
 AC ABB69479;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 35229.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX OS Drosophila melanogaster..
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.
 XX
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR 2001-656860/75.
 DR ABUL13582.
 XX
 PT New Isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions
 XX
 PS Disclosure; SEQ ID NO 35229; 21pp + Sequence Listing; English.
 XX
 The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 useful in developmental biology and in elucidating cell signalling and
 cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL3051), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB5773-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ sequence 796 AA;

XX
 Query Match 67.2%; Score 39; DB 22; Length 796;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 3 DNLLPPRERK 11
 DE :|||||:||:
 DB 786 nnlpprqr 794
 XX
 RESULT 14
 ID AAW79680
 ID AAW79680 standard; Protein; 33 AA.
 XX
 AC AAW79680;
 XX DT 11-JAN-1999 (first entry)
 XX
 DE Synthetic CS198 derived peptide #4.
 XX
 KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human; predisposition; treatment; Barret's oesophagus; gastric ulcer;
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreatitis.
 XX
 OS Synthetic.
 XX
 PN WO9844159-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98WO-US06251.
 XX
 PR 31-MAR-1997; 97US-0828855.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
 PI Gordon J, Granados EN, Hayden M, Hodges SC, Kllass MR;
 PI Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
 PI

XX DR WPI; 1998-542714/46.
 XX PT New gastrointestinal polynucleotides, CS198, and their detection -
 PT used for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis
 XX PS Claim 26; Page 103; 127pp; English.

XX AAW79677-W79680 are synthetic CS198 derived peptide fragments which are
 CC used in a method to detect the presence of a target human CS198
 CC polynucleotide in a test sample. The CS198 gene is useful as a marker
 CC for gastrointestinal (GI) tract disorders. The methods and products can
 CC be used in detecting, diagnosing, staging, monitoring, prognosticating,
 CC preventing or treating, or determining the predisposition to diseases
 CC and conditions of the GI tract, such as GI tract cancer, Barret's
 CC oesophagus, gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease,
 CC ulcerative colitis, and pancreatitis.
 XX Sequence 33 AA;

Query Match 65.5%; Score 38; DB 19; Length 33;
 Best Local Similarity 63.6%; Pred. No. 5.7;
 Matches 7; Conservative 2; Indels 0; Gaps 0;
 Qy 1 SVNDNLPPRERK 11
 111: 11 :11
 Db 3 svdsappgqrk 13

RESULT 15

ID AAE07323 standard; peptide; 33 AA.
 XX AAE07323;
 AC
 XX DT 06-NOV-2001 (first entry)
 XX DE Human CS 198 peptide #4.
 XX KW CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
 KW Barret's oesophagus; gene therapy; drug screening; human.
 XX OS Homo sapiens.
 XX PN US2001010904-A1.
 XX D 02-AUG-2001.
 XX PF 30-MAR-1998; 98US-0050516.
 XX PR 31-MAR-1997; 97US-0828855.

PA (BILL/) BILLING-MEDEL P A.
 PA (COHEN/) COHEN M.
 PA (COLP/) COLPITT S T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSS/) RUSSELL J C.
 PA (STRO/) STROUPE S D.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX

DR WPI; 2001-496163/54.
 XX PT Detecting the presence of target CS 198 polynucleotide, useful for
 PT detecting or diagnosing diseases of the gastrointestinal tract,
 PT comprises contacting test sample with at least one CS 198-specific
 PT polynucleotide
 XX PS Claim 17; Page 52; 68pp; English.

XX The invention relates to a method of detecting the presence of a target
 CC CS 198 polynucleotide comprising contacting the test sample with at
 CC least one CS 198-specific polynucleotide. The method is useful for
 CC detecting diseases of the gastrointestinal (GI) tract organs,
 CC particularly cancer. The CS 198 polynucleotides, polypeptides and
 CC -antibodies are useful for detecting, diagnosing, staging, monitoring,
 CC prognosticating, preventing, treating, or determining predisposition to
 CC diseases and conditions of the GI tract such as cancer, gastric ulcer,
 CC gastritis, Crohn's disease, ulcerative colitis, pancreatitis and
 CC Barrett's oesophagus. The CS 198 polypeptides are useful as standards
 CC or reagents in diagnostic immunoassays, as components or as
 CC target sites for various therapies. Antibodies directed against at
 CC least one epitope contained within these polypeptides are useful as
 CC diagnostic tests and for therapeutic agents, in diagnostic tests and for
 CC screening for conditions or diseases associated with CS 198,
 CC particularly cancer. Monoclonal antibodies may also be used for the
 CC generation of chimeric antibodies for therapeutic use. The CS 198
 CC polynucleotide is also useful in gene therapy and drug screening.
 CC The method of the invention provides an alternative, non-surgical
 CC diagnostic method capable of detecting early stage GI tract disease
 CC such as cancer. The present sequence is a peptide derived from
 CC human CS 198 polypeptide consensus sequence.

XX SQ Sequence 33 AA;
 XX Query Match 65.5%; Score 38; DB 22; Length 33;
 Best Local Similarity 63.6%; Pred. No. 5.7;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 SVDNLPKRK 11
 111: 11 :11
 Db 3 svdsappgqrk 13

Search completed: June 13, 2002, 12:22:22
 Job time: 275 sec

GenCore version 4.5
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OM protein - protein search, using sw model
 Run on: June 13, 2002, 12:17:47 ; Search time 72.45 Seconds
 (without alignments)
 174.775 Million cell updates/sec

Title: US-09-727-739B-3
 Perfect score: 566
 Sequence: 1. MISTRVQCALLLISLALAI.....APRERKAGCKNFFWKIFTFTSC.114
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 747574 seqs, 111073796 residues
 total number of hits satisfying chosen parameters: 747574
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_032802:*

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2: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*

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8: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*

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16: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDSL1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

1. AAU07666 standard; Protein: 114 AA.

ID AAU07666

XX DT 04-DEC-2001 (first entry)

XX DE Rainbow trout preprosomatostatin I (PPSS-I) polypeptide.

XX AC AAU07666;

XX XX Rainbow trout; somatostatin; preprosomatostatin; hypersecretion; PPSS-I; PPSS-II'; PPSS-II'; endocrine tumour; pituitary gland; glucagonoma; AIDS; gastrointeropancreatic tissue; acromegaly; gastrinoma; diabetes mellitus; carcinoid syndrome; cell proliferation; apoptosis; growth hormone; glucagon; acquired immunodeficiency syndrome; neurological disorder; HIV; epilepsy; Alzheimer's disease; Huntington's disease; neuroprotective; neoplasm; metastasis; gene therapy; antidiabetic; nootropic; cytostatic; anti-human immunodeficiency virus; osteopathic; anticonvulsant.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	566	566	100.0	114	22	AAU07666	Rainbow trout prep
2	360		63.6	116	21	AAG03774	Human secreted pro
3	251		44.3	121	3	AAP20028	Sequence of prepro
4	177.5		31.4	115	22	AAU07667	Rainbow trout prep
5	164.5		29.1	111	22	AAU07668	Sequence of prepro
6	162.5		28.7	125	3	AAP20029	Sequence of somato
7	127		22.4	25	3	AAP20198	Somatostatin relat
8	127		22.4	25	22	AAB91017	Somatostatin analo
9	127		22.4	28	19	AAW51859	Mouse somatostatin
10	127		22.4	28	20	AAY28703	Somatostatin peptide
11	127		22.4	28	20	AAY24384	note- "Dibasic cleavage site"

XX PD 03-MAR-1982. 26.115
 XX PF 21-AUG-1981; 81EP-0303825. /note= "Mature PPSS-II"
 XX PR 25-AUG-1980; 80US-0181046. 74
 XX PA (REGC) UNIV OF CALIFORNIA. /note= "Encoded by CAA"
 XX Hobart P, Crawford R, Pictet RL, Rutter WJ.
 PI WPI; 1982-18113E/10.
 XX DR N-PSDB; AAN20033.
 PT New somatostatin and precursors - produced by transformed
 microorganisms
 XX PS Example; Fig 3; 50pp; English.
 XX The inventors claim preprosomatostatin-1, prosomatostatin-1,
 preprosomatostatin-2, prosomatostatin-2 and somatostatin-2; and DNA
 encoding them. The translation of somatostatin mRNA yields a
 precursor (Prepro S1) containing a signal peptide which may be
 released during the transit into the endoplasmic reticulum, and the
 resultant precursor (pro S1) is subsequently cleaved to yield S1
 itself. The prepeptide portion of Prepro S1 is probably about 20-25
 bases long. Translation of PNAS2 predicts the sequence of a 125 AA
 peptide which surprisingly contains a 14 AA sequence at its carboxy
 terminus which differs from S1 by only 2 AAs, and is termed
 CC Somatostatin 2 (S2).
 XX SQ Sequence 121 AA;
 Query Match 44.3%; Score 251; DB 3; Length 121;
 Best Local Similarity 51.3%; Pred. No. 3..6e-20;
 Matches 60; Conservative 15; Mismatches 36; Indels 6; Gaps 4;
 QY 3 STRVOCALA-LLSLALIASSVSAAPSDAKLROLLQRLMAPAGKQELARNLVLE-LLSEL 60
 Db 6 ssrirclvllsitasiscsfaqrdskrlrlhrypl-qqgskqdmtrsalaelllsdl 64
 QY 61 AHYNEAIELDDM--SHGVEQEDVDELELRAPGPVLAPEKAGCKNFEWKFTESC 114
 Db 65 1qgenealeeenfplaeaeggpedahadleraaasggplaprerakgnfwwkftsc 121
 DE -RESULT 4
 ..D AAU07667 standard; Protein; 115 AA.
 XX AC AAU07667;
 XX DT 04-DEC-2001 (first entry)
 DE Rainbow trout preprosomatostatin II (PPSS-II) polypeptide.
 XX KW Rainbow trout; somatostatin; preprosomatostatin; hypersecretion; PPSS-II;
 KW PPSS-II'; preprosomatostatin; pituitary gland; glucagonoma; AIDS;
 KW gastroenteropancreatic tissue; acromegaly; gastrinoma; diabetes mellitus;
 KW carcinoma syndrome; cell proliferation; apoptosis; growth hormone;
 KW glucagon; acquired immunodeficiency syndrome; neurological disorder; HIV;
 KW epilepsy; Alzheimer's disease; Huntington's disease; neuroprotective;
 KW neoplasm; metastasis; gene therapy; antidiabetic; nootropic; cytostatic;
 KW anti-human immunodeficiency virus; osteopathic; anticonvulsant;
 XX OS Oncorhynchus mykiss.
 XX Key Location/Qualifiers
 FT Peptide 1..25 /note= "Signal peptide"
 FT Protein 1..87 /note= "PPSS-II' pre-sequence"

XX Protein 26.115
 PT Misc-difference 74
 XX FT Peptide 88..101 /note= "PPSS-II' pro-sequence"
 XX FT Peptide 88..115 /note= "Prosomatostatin II'"
 XX FT Cleavage-site 100..101 /note= "Dibasic cleavage site"
 XX FT Peptide 102..115 /note= "SS-14 variant peptide"
 XX PN CA2325169-A1.
 XX PD 03-JUN-2001.
 XX PF 01-DEC-2000; 2000CA-2325169.
 XX PR 03-DEC-1999; 99US-01688934.
 XX PA (NDSU-). NDSU RES FOUND.
 XX PI Sheridan MA, Moore CA; Kittelson JD;
 XX DR WPI; 2001-425997/46.
 XX DR N-PSDB; AAS12934.
 PT New somatostatin polypeptides derived from Oncorhynchus mykiss, useful
 PT for treating diabetes mellitus, acromegaly, gastrinoma, acquired
 PT immunodeficiency syndrome and neurological disorders -
 XX PS Claim 2; Fig 3; 52pp; English.
 XX The invention relates to an Oncorhynchus mykiss somatostatin polypeptide
 CC containing a portion of preprosomatostatin I (PPSS-I) and/or a portion of
 CC preprosomatostatin II (PPSS-II). The protein sequences and their
 CC associated polynucleotides are useful for identifying modified
 CC somatostatin polypeptide which functions as a somatostatin agonist useful
 CC for research, therapeutics or diagnostics, including medical and
 CC veterinary applications. The wild-type somatostatin and its modified
 CC version are useful for treating hypersecretion from endocrine tumours in
 CC the pituitary (e.g. acromegaly) or gastroenteropancreatic tissues (e.g.
 CC gastrinoma, glucagonoma, carcinoid syndrome), to cause tumour shrinkage
 CC through their effects on cell proliferation and apoptosis and as adjuncts
 CC in the treatment of diabetes mellitus via inhibition of growth hormone
 CC and glucagon. In addition, dysfunctional somatostatin secretion is
 CC associated with acquired immunodeficiency syndrome (AIDS) and various
 CC neurological disorders (e.g. epilepsy, Alzheimer's disease and
 CC Huntington's disease) and somatostatin antagonists are effective in the
 CC treatment of such conditions. Nucleic acids encoding the polypeptides are
 CC useful in gene therapy and fusion peptides can be targeted to neoplasms
 CC and their metastases, inhibiting the release of their secretory products.
 CC This sequence represents O. Mykiss PPSS-II' protein.
 CC Note: The features for this sequence are specifically claimed in the
 CC specification.
 XX SQ Sequence 115 AA;
 Query Match 31.4%; Score 177.5; DB 22; Length 115;
 Best Local Similarity 34.7%; Pred. No. 5.2e-12;
 Matches 50; Conservative 9; Mismatches 18; Indels 67; Gaps 4;
 QY 5 RVQCALLLSLLAISSVSAAPS---DAKLRLQLRQLSLLMA----- 41
 Db 5 rihsallglalaiscggaaasqpdldrsrlqrraaaalphsgvserwrtfypncp 64
 QY 4.2 -----PAGKQELARNLTVLLSELAHNEAELDDMSHGVQEVDVDELERAPGP 92
 Db 65 clrpkrkvkcpag-----akedlrvelersvgn 91
 QY 93 V-LAPRERKAGCKNEFWKTFSTC 114

CC resultant precursor (pro S1) is subsequently cleaved to yield S1
 CC itself. The prepeptide portion of prepro S1 is probably about 20-25
 CC bases long. Translation of pIaS2 predicts the sequence of a 125 AA
 CC peptide which surprisingly contains a 14 AA sequence at its carboxy
 CC terminus which differs from S1 by only 2 AA's, and is termed
 CC Somatostatin 2 (S2).

XX Sequence 125 AA;

XX SQ Sequence 25 AA;

Query Match 28.7%; Score 162.5; DB 3; Length 25;
 Best Local Similarity 38.9%; Pred. No. 2.7e-10;
 Matches 51; Conservative 16; Mismatches 41; Indels 23; Gaps 6;

QY 1 MLSTRVQCALALLAISSSVSA-----APSDAKLRLQ--LLQRSILMAPAGKQELA 49
 ID 1 mgcicrpailallavlcgpsvssqldreqsdngdldelrqhwllersagslsgews 60
 Db 1 kraveellqmslpeatfqrea--edasmategr--mmlersvdstnnlpprkgc 114

QY 50 RNTLVELLSEL----ARVENEATELDDDMSHGVEQEDVDELERAPGPV--LAPRERKAGC 103
 ID 61 kraveellqmslpeatfqrea--edasmategr--mmlersvdstnnlpprkgc 114

QY 104 KNFFFWKTFFTSC 114
 Db 115 knfywkgftsc 125

QY 14-AUG-1992 (first entry)
 DE Sequence of somatostatin-25 analogue.

KW Somatostatin; hormone; growth hormone release; inhibition.

FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= H-S
 FT Disulfide-bond 14...25
 FT Modified-site 25
 FT /label= C-OH

XX PN US4316891-A.
 D 23-FEB-1982.
 XX PF 14-JUN-1980; 80US-0159801.
 PR 14-JUN-1980; 80US-0159801.
 PA (SALK-) SALK INST BIOLOG.

XX PI Guillemin RCL, Esch FS, Bohlen P, Brazeau PE, Ling NC;
 DR WPI; 1982-19801E/10.

XX PT Extended somatostatin analogues - with increased inhibition of
 PT growth hormone release

XX PS Claim 6; Column 12; 7pp; English.

CC The inventors claim a pharmaceutical compsn. which comprises (i)
 CC synthetic somatostatin-28 (SS-28), SS-25 or (D-Trp(22))-SS-28 and
 CC (ii) a liq. or solid carrier, and SS-28 derivs. and SS-25 derivs.
 CC The compsn. and derivs. are more potent than somatostatin in
 CC inhibiting release of growth hormone; they also inhibit basal and
 CC stimulated insulin and glucagon secretion (D-Trp(22))-SS-28
 CC exhibits very substantial increases in potency w.r.t. inhibition of
 CC growth hormone secretion.

Query Match Score 127; DB 22; Length 25;
 Best Local Similarity 91.3%; Pred. No. 3e-07;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 92 PVLAPRERKAGCKNFEWKTFETSC 114
 ID AAW51859 standard; peptide; 28 AA.
 XX 3 pamaprkagcknfwkftftsc 25

RESULT 9
 AAW51859

ID AAW51859 standard; peptide; 28 AA.
 XX 1 :||||| :||||| :||||| :|||||

Db 3 pamaprkagcknfwkftftsc 25

DE 10-SEP-1998 (first entry)

XX Somatostatin analogue for the treatment of syndrome X of Reaven.

XX Somatostatin analogue; syndrome X of Reaven; hyperinsulinaemia syndrome;

XX diazoxide; cyclothiazide; metformin.

XX Synthetic.

XX WO9810786-A2.

XX 19-MAR-1998.

XX 10-SEP-1997; 97WO-IL00301.

XX 10-OCT-1996; 96IL-0119403.

XX 12-SEP-1996; 96IL-0119250.

XX PA (COHE/) COHEN Y.

XX PI Cohen Y;

XX DR; 1998-271636/24.

XX Composition for treatment of the risk factors of syndrome X of Reaven - (hyperinsulinaemia syndrome) comprises somatostatin, diazoxide, cyclothiazide (or their analogues) and/or metformin

XX PS; Page 41; 45pp; English.

XX The invention relates to a pharmaceutical composition for treatment of the risk factors of syndrome X of Reaven (hyperinsulinaemia syndrome). It comprises somatostatin, diazoxide, cyclothiazide (or an analogue of one of these) or metformin as the active ingredient. The composition reduces resistance to insulin, and so treats and prevents all the associated risk factors at once. The risk factors are hypertension, dyslipidaemia (raised triglyceride and LDL levels with reduced HDL levels), shorter coagulation time due to increased Plasminogen Activator Inhibitor-1 levels, core obesity, glucose intolerance hyperinsulinaemia. The composition reduces the incidence of ischaemic heart disease, cerebrovascular disorders, intermittent claudication, ischaemic bowel disease, impotence due to peripheral vascular disease, hypercoagulation (e.g. renal vein thrombosis), obesity and glucose intolerance. The present sequence represents a specifically claimed somatostatin analogue.

XX SQ Sequence 28 AA;

XX Query Match Score 127; DB 20; Length 28;
 Best Local Similarity 91.3%; Pred. No. 3.5e-07;
 Matches 21; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 92 PVLAPRERKAGCKNFEWKTFETSC 114

DB 6 pamaprkagcknfwkftftsc 28

Query Match Score 127; DB 19; Length 28;

Best Local Similarity 91.3%; Pred. No. 3.5e-07;

Matches 21; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 92 PVLAPRERKAGCKNFEWKTFETSC 114

DB 6 pamaprkagcknfwkftftsc 28

RESULT 10

AY28703 standard; peptide; 28 AA.

ID AY28703;

AC AY28703;

XX DT 07-OCT-1999 (first entry).

XX XX DE Mouse somatostatin SS-28 hormone.

XX KW Mouse somatostatin SS-28 hormone; growth hormone; insulin; glucagon;

XX KW thyroid stimulating hormone; octreotide; cell-based delivery of insulin;

XX KW glucose-stimulated insulin secretion; SSTRV; somatostatin receptor type-V gene; diabetes.

XX OS Mus musculus.

XX FN WO9935242-A1.

XX PD 15-JUL-1999.

XX PF 11-JAN-1999;

XX XX PR 03-JUN-1998;

XX PR 03-JUN-1998; 98US-0087848.

XX PR 12-JAN-1998; 98US-0071193.

XX PR 12-JAN-1998; 98US-0071209.

XX PR 12-JAN-1998; 98US-0072556.

XX PR 03-JUN-1998; 98US-0087821.

XX PA (BETA-) BETAGENE INC.

XX PI Clark SA, Quaade C;

XX DR WPI; 1999-444195/37.

XX PT New defined medium for culture of neuroendocrine cells, e.g. of

PT insulin-secreting cells.

XX PS Example 8; Page 143; 312pp; English.

XX CC The present sequence is a mouse somatostatin (SS-28) hormone which

CC was found to inhibit the release of growth hormone, thyroid stimulating

CC hormone, insulin and glucagon. In addition, SS-28 and its analogue

CC Octreotide may inhibit growth of some tumours. The hormone was

CC used to study its effect on glucose-stimulated insulin secretion in

CC high expressing and non-expressing clones of mouse somatostatin

CC receptor, type V gene (SSTRV). The insulin secretion was highly inhibited

CC in the high expressing clone as compared to the non-expressing clone

CC because the high expressing clone showed high sensitivity to

CC somatostatin. The hormone effectively inhibits insulin secretion in the

CC absence of glucose. The somatostatin receptor can be introduced in cell

CC lines, used in cell-based delivery of insulin for treating diabetes, for

CC precise regulation of insulin release.

XX SQ Sequence 28 AA;

XX Query Match Score 127; DB 20;

XX Best Local Similarity 91.3%; Pred. No. 3.5e-07;

XX Matches 21; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 92 PVLAPRERKAGCKNFEWKTFETSC 114

DB 6 pamaprkagcknfwkftftsc 28

RESULT 11

AY24384

ID AY24384 standard; peptide; 28 AA.

AC AY24384;

XX XX

XX DT 20-SEP-1999 (first entry)

DE Synthetic.

XX Somatostatin peptide hormone SS-28.

KW Glucagon-like peptide I receptor; GIP-1 receptor; drug screening;

KW secretory function; immortalised neuroendocrine secretory cell;

KW regulation; diabetes; insulin secretion; neuroendocrine-based disorder;

KW Parkinson's disease; athyrotic, cretinism; Addison's disease.

XX OS Mus musculus.

XX WO9935495-A2.

XX 15-JUL-1999.

PD XX 11-JAN-1999; 99WO-US00631.

PF XX PR 03-JUN-1998; 98US-0087848.

PR 12-JAN-1998; 98US-0071193.

PR 12-JAN-1998; 98US-0071209.

PR 12-JAN-1998; 98US-0072556.

PR 03-JUN-1998; 98US-0087821.

PA XX (BETA-) BETAGENE INC.

XX PR 03-JUN-1998; 98US-0087848.

PI XX Clark SA, Thigpen AE;

XX WPI; 1999-419351/35.

PT XX New immortalized neuroendocrine cells that stably secrete polypeptide, particularly used to treat diabetes and hypoglycaemia

PT XX Example 8; Page 148; 318pp; English.

PS XX The present invention describes immortalized neuroendocrine cells (A) that stably secrete a polypeptide hormone (I) contain an expression region that includes a transgene (TG), linked to a promoter functional in eukaryotic cells, such that expression of TG increases sensitivity of the cells to a modulator of (I) secretion. (A) are specifically used, by transplantation, to treat diabetes or hypoglycaemia (especially where associated with insulin therapy) but more generally are used to express, *in vivo*, a wide range of therapeutic hormones, enzymes, amidated proteins and growth factors. Also engineered neuroendocrine cells are used to identify new therapeutic agents or drug targets.

CC (A) have a stable phenotype and particularly inducible glucagon secretion and glucose counter-regulatory capacities, i.e. they balance the hyperglycaemic effects of beta-cell loss and the hypoglycaemic effects of administered insulin. Since they are of human origin, they are less likely to suffer immune rejection than xenografts. The present sequence represents the peptide hormone somatostatin SS-28 used in an example from the present invention.

SQ XX Sequence 28 AA;

CC Query Match 22.4%; Score 127; DB 20; Length 28;

CC Best Local Similarity 91.3%; Pred. No. 3.5e-07;

CC Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CC

QY XX 92 PVLAPRERKAGCKNFFWKTFTSC 114

DB XX 1 : ||| ||| ||| ||| ||| |||

DB 6 pamaprerkagcknffwktftsc 28

RESULT 13

ID XX AAB91018

ID XX AAB91018 standard; Peptide; 28 AA.

XX AC AAB91018;

XX DT 22-JUN-2001 (first entry)

DE XX Somatostatin related Peptide SEQ ID NO:192.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;

XX blood component; modification; succinimidyl; maleimido group; amino;

XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS XX Synthetic.

OS XX WO200069900-A2.

XX PD 23-NOV-2000.
 XX PF 17-MAY-2000; 2000WO-US13576.
 XX PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX PA (CONJ-) CONJUCHEM INC.
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 DR WPI; 2001-112059/12.
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT Disclosure; Page 252; 733pp; English.
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB9029 to AAB9241 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX SQ Sequence 28 AA;

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB9029 to AAB9241 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX SQ Sequence 28 AA;

Query Match 22.4%; Score 127; DB 22; Length 28;
 Best Local Similarity 91.3%; Pred. No. 3.5e-07;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 92 PVLAPRERKAGCKNFFFWKTFKFTSC 114
 :|||||||||:|||||:|||||:|||||:
 6 pamaprkagcknffwktftsc 28

RESULT 14
 AAU07669 ID AAU07669 standard; Peptide: 28 AA.
 XX AC AAU07669;
 XX DT 04-DEC-2001 (first entry)
 XX DE Mammalian somatostatin 28 (SS-28) peptide sequence.

XX DE Rainbow trout; somatostatin; preprosomatostatin; hypersecretion; PPSS-I;
 KW PPSS-II'; PPSS-II'; endocrine tumour; pituitary gland; glucagonoma; AIDS;
 KW gastroenteropancreatic tissue; acromegaly; gastrinoma; diabetes mellitus;
 KW carcinoid syndrome; cell proliferation; apoptosis; growth hormone; SS-28;
 KW glucagon; acquired immunodeficiency syndrome; neurologic disorder; HIV;
 KW epilepsy; Alzheimer's disease; Huntington's disease; gene therapy; neuroprotective;
 KW neoplasm; metastasis; neurotrophic; cytosolic;
 KW anti-human immunodeficiency virus; osteopathic; anticonvulsant.
 XX OS Mammalia sp.
 PN CA2325169-A1.

XX PD 03-JUN-2001.
 XX PF 01-DEC-2000; 2000CA-2325169.
 XX PR 03-DEC-1999; 99US-0168934.
 XX PA (NDSU-) NDSU RES FOUND.
 XX PI Sheridan MA, Moore CA, Kittelson JD;
 XX DR WPI; 2001-425997/46.
 XX PT New somatostatin polypeptides derived from Oncorhynchus mykiss, useful
 PT for treating diabetes mellitus, acromegaly, gastrinoma, acquired
 PT immunodeficiency syndrome and neurological disorders -
 XX PS Example 5; Fig 6; 52pp; English.
 XX CC The invention relates to an Oncorhynchus mykiss somatostatin polypeptide
 CC containing a portion of preprosomatostatin I (PPSS-I) and/or a portion of
 CC preprosomatostatin II (PPSS-II). The protein sequences and their
 CC associated polynucleotides are useful for identifying modified
 CC somatostatin polypeptide which functions as a somatostatin agonist useful
 CC for research, therapeutics or diagnostics, including medical and
 CC veterinary applications. The wild-type somatostatin and its modified
 CC version are useful for treating hypersecretion from endocrine tumours in
 CC the pituitary (e.g. acromegaly) or gastroenteropancreatic tissues (e.g.
 CC gastrinoma, glucagonoma, carcinoid syndrome), to cause tumour shrinkage
 CC through their effects on cell proliferation and apoptosis and as adjuncts
 CC in the treatment of diabetes mellitus via inhibition of growth hormone
 CC and glucagon. In addition, dysfunctional somatostatin secretion is
 CC associated with acquired immunodeficiency syndrome (AIDS) and various
 CC neurological disorders (e.g. epilepsy, Alzheimer's disease and
 CC Huntington's disease) and somatostatin antagonists are effective in the
 CC treatment of such conditions. Nucleic acids encoding the polypeptides are
 CC useful in gene therapy and fusion peptides can be targeted to neoplasms
 CC and their metastases, inhibiting the release of their secretory products.
 XX SQ Sequence 28 AA;

Query Match 22.4%; Score 127; DB 22; Length 28;
 Best Local Similarity 91.3%; Pred. No. 3.5e-07;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 92 PVLAPRERKAGCKNFFFWKTFKFTSC 114
 :|||||||||:|||||:|||||:
 6 pamaprkagcknffwktftsc 28

RESULT 15
 AAB91020 ID AAB91020 standard; Peptide: 29 AA.
 XX AC AAB91020;
 XX DT 22-JUN-2001 (first entry)
 DE Somatostatin related peptide SEQ ID NO:194
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200069900-A2.
 XX PD 23-NOV-2000.
 XX

PF 17-MAY-2000; 2000WO-US13576.
 XX PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 XX

PS Disclosure; Page 253; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB9241 represent peptides which can be used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 29 AA;

Query Match 22.4%; Score 127; DB 22; Length 29;
 Best Local Similarity 91.3%; Pred. No. 3.7e-07;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 92 PVLAPRKAGCKNFFWKTFTSC 114
 | :||||| :||||| :|||||
 Db 7 pamaprkagcknffwktftsc 29

Search completed: June 13, 2002, 12:22:20
 Job time: 273 sec

QY 67 AIEELDDMSHGVEQEDVLELERA--PGPVLAPEPRKAGCKNFFWKTFTSC 114
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 61 ALEPEDLPQAAEQDEMRLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC 110

RESULT 2
 US-08-648-322-2
 Sequence 2, Application US/08648322
 GENERAL INFORMATION:
 APPLICANT: Sutcliffe, Gregor J.
 APPLICANT: de Lecea, Luis
 TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,
 TITLE OF INVENTION: COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
 STREET: 10666 NO. 6074872th Torrey Pines Road, TPC-8
 CITY: La Jolla
 STATE: California
 COUNTRY: US
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09-001, 472
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/033, 980
 FILING DATE: 31-DEC-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/037, 386
 FILING DATE: 07-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36, 688
 REFERENCE/DOCKET NUMBER: 1488.0430002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-09-001-472-3

NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34, 163
 REFERENCE/DOCKET NUMBER: 519.0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-6312
 TELEFAX: (619) 554-2937
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-08-648-322-2

RESULT 3
 US-09-001-472-3
 Sequence 3, Application US/09001472
 GENERAL INFORMATION:
 APPLICANT: OLSEN, HENRIK S.
 APPLICANT: RUBEN, STEVEN M.
 TITLE OF INVENTION: CORTISTATIN POLYPEPTIDES
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON
 STATE: DC
 COUNTRY: US
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09-001, 472
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/033, 980
 FILING DATE: 31-DEC-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/037, 386
 FILING DATE: 07-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36, 688
 REFERENCE/DOCKET NUMBER: 1488.0430002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-09-001-472-3

RESULT 4
 US-08-455-970A-10
 Sequence 10, Application US/08455970A
 GENERAL INFORMATION:
 Patent No. 5708155
 APPLICANT: POTTER, ANDREW A.
 APPLICANT: REDMOND, MARK J.
 APPLICANT: HUGHES, HUW P.A.
 TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN CHIMERAS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: REED & ROBINS
 STREET: 285 HAMILTON AVENUE, SUITE 200
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 94301
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455, 970A

Query Match 16.7%; Score 94.5%; DB 4; Length 112;
 Best Local Similarity 33.0%; Pred. No. 0.00055;
 Matches 37; Conservative 13; Mismatches 43; Indels 19; Gaps 6;

QY 9 ALALLSLLAASSV--SAAPSDAKLROLLQSLMAPAGK--QELARNTLVELLSELAVH 63
 Db 13 ALSLL-LLLLSGIIAASALPES-----GPTGQDSVQDATGGRTGLTFLAWN 60

QY 64 ENEAIEELDDMSHGVEQEDVLELERAAPGPVLAPEPR-KAGCKNFFWKTFTSC 114
 Db 61 HEWASQ-DSSSTAPEGGTPELSKRQERPLQPPHRDKKKPCKKNFFWKTFTSSC 111

Query Match 16.7%; Score 94.5%; DB 3; Length 112;
 Best Local Similarity 33.0%; Pred. No. 0.00055;
 Matches 37; Conservative 13; Mismatches 43; Indels 19; Gaps 6;

QY 9 ALALLSLLAASSV--SAAPSDAKLROLLQSLMAPAGK--QELARNTLVELLSELAVH 63
 Db 13 ALSLL-LLLLSGIIAASALPES-----GPTGQDSVQDATGGRTGLTFLAWN 60

QY 64 ENEAIEELDDMSHGVEQEDVLELERAAPGPVLAPEPR-KAGCKNFFWKTFTSC 114
 Db 61 HEWASQ-DSSSTAPEGGTPELSKRQERPLQPPHRDKKKPCKKNFFWKTFTSSC 111

Query Match 16.7%; Score 94.5%; DB 3; Length 112;
 Best Local Similarity 33.0%; Pred. No. 0.00055;
 Matches 37; Conservative 13; Mismatches 43; Indels 19; Gaps 6;

QY 9 ALALLSLLAASSV--SAAPSDAKLROLLQSLMAPAGK--QELARNTLVELLSELAVH 63
 Db 13 ALSLL-LLLLSGIIAASALPES-----GPTGQDSVQDATGGRTGLTFLAWN 60

QY 64 ENEAIEELDDMSHGVEQEDVLELERAAPGPVLAPEPR-KAGCKNFFWKTFTSC 114
 Db 61 HEWASQ-DSSSTAPEGGTPELSKRQERPLQPPHRDKKKPCKKNFFWKTFTSSC 111

FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-00016.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-08-455-970A-10

SULT 5
-07-977-628A-1
Sequence 1, Application US/07977628A
Patent No. 5405597
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Lister-James, John
APPLICANT: ~~REDACTED~~

ALLEGRETTI, Scott, Dattam, Somato
TITLE OF INVENTION: Technetium-99m Labeled Somato
TITLE OF INVENTION: Derived Peptides for Imaging
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/977,628A

FILING DATE: 17-NOV-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5405597nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 91,642-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 2..14
 OTHER INFORMATION: /label= Disulfide-bond
 OTHER INFORMATION: /note= "The sidechain thiol groups of the third
 OTHER INFORMATION: residue-cysteine and the carboxy-terminal cysteine
 OTHER INFORMATION: form a disulfide bond in native somatostatin
 US-07-977-628A-1

Query Match 15.4%; Score 87; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 101 AGCKNFWKTFSC 114
 ||||| ||||| |||||
 Db 1 AGCKNFWKTFSC 14

RESULT 6
US-08-255-272-5
Sequence 5, Application US/08255272
Patent No. 5627268
GENERAL INFORMATION:
APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Khoury-Christiansen, Anastasia
APPLICANT: M.
TITLE OF INVENTION: Production of Therapeutic Peptides in
Transgenic Animals as a Fusion with Hemocytobin
TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,272
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 6794-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids

TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-255-272-5

Query Match 15.4%; Score 87; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 14; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 101 AGCKNFEWKTFTSC 114
 |||||||

RESULT 7
 US-08-416-007-4
 Sequence 4, Application US/08416007
 Patent No. 5693679

GENERAL INFORMATION:
 APPLICANT: Vincent, Jean-Pierre
 APPLICANT: Baudet, Alain
 TITLE OF INVENTION: FLUORESCENT SOMATOSTATIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/676, 263
 FILING DATE: 07-NOV-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94300224.6
 FILING DATE: 12-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharp, Jeffrey S.
 REGISTRATION NUMBER: 31,879
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: (312) 474-6600

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Cross-links
 LOCATION: 3...14
 US-08-676-263-11

Query Match 15.4%; Score 87; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AGCKNFFWKTFSTSC 114
 Db 1 AGCKNFFWKTFSTSC 14

RESULT 8
 US-08-676-263-11:
 Sequence 11, Application US/08676263
 Patent No. 5705143

GENERAL INFORMATION:
 APPLICANT: Bower, Gary R.
 APPLICANT: Forster, Alan M.
 APPLICANT: Riley, Anthony L. M.
 APPLICANT: Storey, Anthony E.
 TITLE OF INVENTION: BIOLOGICAL TARGETING AGENTS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker Drive/6300 Sears Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America

ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/676, 263
 FILING DATE: 07-NOV-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94300224.6
 FILING DATE: 12-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharp, Jeffrey S.
 REGISTRATION NUMBER: 31,879
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: (312) 474-6600

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Cross-links
 LOCATION: 3...14
 US-08-676-263-11

Query Match 15.4%; Score 87; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AGCKNFFWKTFSTSC 114
 Db 1 AGCKNFFWKTFSTSC 14

RESULT 9
 US-08-286-748B-13
 Sequence 13, Application US/08286748B
 Patent No. 5759542

GENERAL INFORMATION:
 APPLICANT: VICTOR Gurewich
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
 TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
 TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50Z or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,748B
 FILING DATE: August 5, 1994
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: J. Peter Fasse

REGISTRATION NUMBER: 32,983
 REFERENCE/DOCKET NUMBER: 04547/013001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-286-748B-13

Query Match 15.4%; Score 87; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 AGCKNFWKTFKTFSC 114

RESULT 10
 US-08-690-090A-1
 Sequence 1, Application US/08690090A
 Patent No. 5770687
 GENERAL INFORMATION:
 APPLICANT: HORNIK, VERED
 APPLICANT: SERI-LEVY, ALON
 APPLICANT: GELLERMAN, GARY
 APPLICANT: GILON, CHAIM
 TITLE OF INVENTION: Conformationally Constrained Backbone
 TITLE OF INVENTION: Cyclized Somatostatin Analogs
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,159
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Fanucci, Allan A.
 REGISTRATION NUMBER: 30,256
 REFERENCE/DOCKET NUMBER: 7754-0333
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-488-159-1
 Query Match 15.4%; Score 87; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 AGCKNFWKTFKTFSC 114
 RESULT 12
 US-08-465-764-1
 Sequence 1, Application US/08465764
 Patent No. 5814298
 GENERAL INFORMATION:
 APPLICANT: Lister-James, John
 APPLICANT: Dean, Richard T
 TITLE OF INVENTION: Technetium-99m Labeled
 Somatostatin-Derived Peptides for Imaging and Therapeutic
 Uses
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 US-08-690-090A-1

Query Match 15.4%; Score 87; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 AGCKNFWKTFKTFSC 114
 RESULT 11
 US-08-488-159-1
 Sequence 1, Application US/08488159
 Patent No. 5811392
 GENERAL INFORMATION:
 APPLICANT: GILON, Chaim
 TITLE OF INVENTION: Conformationally Constrained Backbone
 TITLE OF INVENTION: Cyclized Peptide Analogs
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,159
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Fanucci, Allan A.
 REGISTRATION NUMBER: 30,256
 REFERENCE/DOCKET NUMBER: 7754-0333
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

ADDRESSEE: Banner & Allegretti, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,764
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 5814298man, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,385-R
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEFAX: 312-715-1234
 TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: circular
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 3..14
 OTHER INFORMATION: /label- Disulfide bond
 OTHER INFORMATION: /note- "The peptide is cyclized between the sidechain sulfur atoms of the 3d and 14th residues
 OTHER INFORMATION: US-08-465-764-1

Query Match 15.4%; Score 87; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AGCKNFFWKTFSTC 114
 Db 1 AGCKNFFWKTFSTC 14

RESULT 13
 -08-475-751-4
 Sequence 4, Application US/08475751
 Patent No. 5824772

GENERAL INFORMATION:
 APPLICANT: Vincent, Jean-Pierre
 APPLICANT: Gaudriault, Georges
 APPLICANT: Beaudet, Alain
 TITLE OF INVENTION: FLUORESCENT SOMATOSTATIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Clark & Elbing LLP
 STREET: 585 Commercial Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-1024

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/475,751
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/416,007
 FILING DATE: 04-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06942/004001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/723-4123
 TELEFAX: 617/723-8962

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-475-751-4

Query Match 15.4%; Score 87; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AGCKNFFWKTFSTC 114
 Db 1 AGCKNFFWKTFSTC 14

RESULT 14
 US-08-282-980B-1
 Sequence 1, Application US/08282980B
 Patent No. 5932189

GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 APPLICANT: McBride, William
 APPLICANT: Lister-James, John
 TITLE OF INVENTION: Peptides
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff.
 STREET: 300 South Wacker Drive, Seventh Floor
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/282,980B
 FILING DATE: 29-JUL-1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 5932189nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,385-I
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-913-0001
 TELEFAX: 312-913-0002
 TELEX:

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: circular
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 3..14

; OTHER INFORMATION: /label- Disulfide bond
; OTHER INFORMATION: /note- "A disulfide bond exists between the
; OTHER INFORMATION: two sulfur atoms of the cysteine residues;
; US-08-282-980B-1

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Query Match 15.48; Score 87; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0

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RESULT 15
US-08-747-137-13
Sequence 13, Application US/08747137
Patent No. 5945033
GENERAL INFORMATION:
APPLICANT: YEN, Richard C.K.
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,831
FILING DATE: 01-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-000840US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant

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Query Match 15.4%; Score 87; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0
Query 101 AGCKNEFWKTFTSC 114
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 13, 2002, 12:20:22 ; search time 35.79 seconds
(without alignments)

306.068 Million cell updates/sec

Title: US-09-727-739B-3

Perfect score: 566

Sequence: 1 MLSTRYQCALALLSALAI.....APRKAGCKNEFWKTFSTC 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	409	72.3	114	1 RIIDS1	somatostatin-14 pr
2	409	72.3	114	2 I50798	preprosomatostatin
3	400	70.7	116	1 S20630	somatostatin precu
4	382.5	67.6	115	2 JC6166	somatostatin-14 pr
5	360	63.6	116	1 RIHUS1	somatostatin I pre
6	360	63.6	116	1 A28968	somatostatin I pre
7	352	62.2	116	1 RIBOS1	somatostatin precu
8	347	61.3	116	1 RIRTS1	somatostatin precu
9	347	61.3	116	1 RIMSS1	somatostatin precu
10	293	51.8	92	1 RIGPS	somatostatin I pre
11	251	44.3	121	1 RIAFS1	somatostatin I pre
12	177.5	31.4	115	2 I51064	somatostatin II pr
13	162.5	28.7	125	1 RIAFS2	somatostatin II pr
14	127	22.4	28	2 A61322	somatostatin-28 -
15	116.5	20.6	34	2 A32271	somatostatin-II relat
16	114	20.1	73	2 S00169	somatostatin II pr
17	110.5	19.5	105	1 RIIDS2	somatostatin-22 pr
18	107.5	19.0	103	2 JC6167	somatostatin-14 [P
19	107	18.9	25	2 A60842	somatostatin, panc
20	106	18.7	37	2 A32000	somatostatin II pr
21	103.5	18.3	74	2 S00166	cortistatin precu
22	94.5	16.7	112	2 S67489	somatostatin - sli
23	87	15.4	14	2 C60414	somatostatin I - C
24	87	15.4	14	2 B60842	somatostatin I - E
25	87	15.4	14	2 A60840	somatostatin I - S
26	87	15.4	14	2 S00172	somatostatin-25 -
27	87	15.4	25	2 B60840	cortistatin-like p
28	86.5	15.3	105	2 JC5414	somatostatin - spo
29	82	14.5	14	2 A60622	

30 79.5 14.0 846 2 S52418
31 77.5 13.7 571 2 AE3281
32 77 13.6 385 2 T18821
33 74 13.1 297 2 T48855
34 74 13.1 965 2 AE0418
35 74 13.1 1385 2 T13887
36 74 13.1 1389 2 T13852
37 74 13.1 1732 2 T14039
38 73 12.9 493 2 S49175
39 72.5 12.8 216 2 T40268
40 72.5 12.8 274 2 S72643
41 71.5 12.6 1285 2 H85041
42 71 12.5 1295 2 T24587
43 70.5 12.5 478 2 AB3641
44 70.5 12.5 925 2 E83529
45 70 12.4 414 2 T15947

ALIGNMENTS

RESULT
RIIDS1
Somatostatin-14 precursor - channel catfish
N; Alternate names: somatostatin-14
C; Species: Ictalurus punctatus (channel catfish)
C; Date: 30-Jun-1980 #sequence_revision 31-Dec-1993 *text_change 18-Jun-1999
C; Accession: S00292; A93897; A01435
R; Minth, C.D.; Taylor, W.L.; Magazin, M.; Collier, K.; Weith, H.L.; Dixon, J.E.
J. Biol. Chem. 257, 10372-10377, 1982
A; Title: The structure of cloned DNA complementary to catfish pancreatic somatostatin
A; Reference number: S00292; MUID:82265698
A; Accession: S00292
A; Molecule type: mRNA
A; Residues: 82-108 <TAY>
A; Cross-references: GB:J00944
R; Andrews, P.C.; Dixon, J.E.
J. Biol. Chem. 256, 8267-8270, 1981
A; Title: Isolation and structure of a peptide hormone predicted from a mRNA sequence
A; Reference number: A92334; MUID:81264223
A; Accession: A92334
A; Molecule type: Protein
A; Residues: 101-114 <AND>
C; Superfamily: somatostatin
C; Keywords: neuropeptide
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-100/Domain: propeptide #status predicted <PRO>
F; 101-114/Product: somatostatin-14 #status experimental <MAT>
F; 103-114/Disulfide bonds: #status experimental
Query Match 72.3%; Score 409; DB 1; Length 114;
Best Local Similarity 69.3%; Pred. No. 4.5e-32;
Matches 79; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MLSTRQCALALLSALAISSVSAAPSDAKLQLQLQRLMAPAGKQELARNTLVELLSEL 60
DB 1 MPSTRQCALALLSALAVSVCSSGAPSDAKLROFLRQSLAPSVKQELRTYTLAEL 60

QY 61 AHVENEAEIELDDMSHGVEQEDVDELELERAAPGVPVLAAPRERKAGCKNFFWKTETSC 114
DB 61 AQAENEVLDSDEVRAAESEGARLEMERAAGPMLAPRERKAGCKNFFWKTETSC 114

RESULT 2
 I50798
 preprosomatostatin SS-14 - channel catfish
 C;Species: Ictalurus punctatus (channel catfish)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C;Accession: I50798
 R;Dixon, J.E.; Andrews, P.C.
 Adv. Exp. Med. Biol. 188, 19-29, 1985
 A;Title: Somatostatins of the channel catfish.
 A;Reference: I50798; MUID:85303576
 A;Accession: I50798
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: mRNA
 A;Residues: 1-114 <DIX>
 A;Cross-references: GB:M25903; NID:9213339; PIDN:AAA49339.1; PID:9213340
 C;Superfamily: somatostatin

Query Match 72.3%; Score 409; DB 2; Length 114;
 Best Local Similarity 69.3%; Pred. No. 4.5e-32;
 Matches 79; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MLSTRVOCALLSLALAISVSAAPSDAKLROLLQRLSLMAPAGKQELARNTLVELLSEL 60
 Db 1 MPSTRQCALLALLAVALSVCVSGAPSDAKLROLFLQSLAPSVKQELTRYLAEELAEL 60

Query Match 70.7%; Score 400; DB 1; Length 116;
 Best Local Similarity 69.8%; Pred. No. 3.4e-31;
 Matches 81; Conservative 14; Mismatches 19; Indels 2; Gaps 1;

Qy 1 MLSTRVOCALLSLALAISVSAAPSDAKLROLLQRLSLMAPAGKQELARNTLVELLSEL 60
 Db 1 MLSCLRQCALLALLSLALAIVGTVSAAAPSDPRLQFLQKSLAAAAGKQELAKYFLAEELLSEP 60

Query Match 67.6%; Score 382.5; DB 2; Length 115;
 Best Local Similarity 69.0%; Pred. No. 1.6e-29;
 Matches 80; Conservative 13; Mismatches 20; Indels 3; Gaps 2;

Qy 1 MLSTRVOCALLSLALAISVSAAPSDAKLROLLQRLSLMAPAGKQELARNTLVELLSEL 60
 Db 1 MQSCRVQCALLLISLALAINSSAAPTDPRLQFLQKSL-ASAGKQELAKYFLAEELLSEP 59

Query Match 61 AHVNEAIEFLDDMSHGVQEDVDILELEERA-PGPVLAPRERKAGCKNFFWKTFSC 114
 Best Local Similarity 60.5%; Pred. No. 1.6e-28;
 Matches 60; Conservative 14; Mismatches 19; Indels 2; Gaps 2;

Qy 1 SOTDNEALESDDLPRGAEQDEVRLERSANSSPALAPRERKAGCKNFFWKTFSC 115

RESULT 5

RIHUS1

somatostatin I precursor - human
 N;Alternate names: preprosomatostatin
 N;Contains: somatostatin 14 (SS-14); somatostatin 28 (SS-28)
 C;Species: Homo sapiens (man)
 C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 18-Jun-1999
 C;Accession: A43614; MUID:809381; S50024
 A;Molecule type: DNA
 A;Residues: 1-116 <SH2>
 A;Cross-references: GB:J00306; NID:9338287; PIDN:AAA60566.1; PID:9338288
 R;Shen, L.P.; Pictet, R.L.; Rutter, W.J.
 Proc. Natl. Acad. Sci. U.S.A. 79, 4575-4579, 1982
 A;Title: Human somatostatin I: sequence of the cDNA.
 A;Reference number: A43614; MUID:84146798
 A;Accession: A01430
 A;Molecule type: mRNA
 A;Residues: 1-116 <SHE>
 A;Cross-references: GB:J00306; NID:9338287; PIDN:AAA60566.1; PID:9338288
 A;Experimental source: pancreatic somatostatinoma
 R;Gomez, S.; Boileau, G.; Zollinger, L.; Nault, C.; Rholam, M.; Cohen, P.
 EMBO J. 8, 2911-2916, 1989
 A;Title: Site-specific mutagenesis identifies amino acid residues critical in prohormone processing
 A;Reference number: S09381; MUID:90059875
 A;Accession: S09381
 A;Molecule type: mRNA
 A;Residues: 88-108 <GOM>
 R;Odum, L.; Johnsen, A.H.
 Biochem. J. 303, 263-268, 1994
 A;Title: Human seminal plasma contains somatostatin-64.
 A;Reference number: S50024; MUID:95031969
 A;Accession: S50024
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 53-62-67-82 <ODU>
 C;Comment: Somatostatin inhibits the release of somatotropin.
 C;Genetics:
 A;Gene: GDB:SST
 A;Cross-references: GDB:119604; OMIM:182450
 A;Map position: 3q28-3q28
 A;Introns: 46/3
 C;Function:
 A;Reference number: JC6166; MUID:97057290

RESULT 4

JC6166
 somatostatin-14 precursor - laughing frog
 N;Alternate names: PSS1 protein
 C;Species: Rana ridibunda (laughing frog)
 C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999
 C;Accession: JC6166
 R;Tostivint, H.; Lihrmann, I.; Bucharles, C.; Vieuau, D.; Coulouarn, Y.; Fournier, A.; Cocco, A.;
 Proc. Natl. Acad. Sci. U.S.A. 93, 12605-12610, 1996
 A;Title: Occurrence of two somatostatin variants in the frog brain: Characterization of
 A;Reference number: JC6166; MUID:97057290

AA; Description: inhibits the secretion of a number of peptide hormones, including somatotropin
CC; Superfamily: somatostatin
CC; Keywords: hormone; hypothalamus; neuropeptide
FF; 1-24/Domain: signal sequence #status predicted <SIG>
FF; 25-88/Domain: propeptide #status predicted <PRO>
FF; 89-116/Product: somatostatin-28 #status predicted <M28>
FF; 103-116/Product: somatostatin-14 #status predicted <M14>
FF; 105-116/Disulfide bonds: #status experimental

A; Reference number: A40929; MUID:88288237
A; Accession: A40929
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-116 <SUA>
A; Cross-references: GB:M31217; NID:g16363
A; Note: the authors translated the codon
C; Comment: Somatostatin inhibits the rele-

Query	Match	Score
C/Keywords: hormone; neuropeptide	62.2%	3
F; 1-24/Domain: signal sequence #status . pred	61.2%	Pred. N
F; 25-88/Domain: propeptide #status pred	71	Mism
F; 89-116/Product: somatostatin-28 #status		
F; 103-116/Product: somatostatin-14 #status		
F; 105-116/Disulfide bonds: #status predic		

RESULT 6
A28968
somatostatin I precursor - crab-eating macaque
N;Alternate names: Preprosomatostatin
N;Contains: somatostatin 14 (SS-14); somatostatin 28 (SS-28)
C;Species: *Macaca fascicularis* (crab-eating macaque)
C;Date: 30-Jun-1989 #sequence_revision 31-Jan-1997 #text_change 18-Jun-1999
C;Accession: A28968
R;Travis, G.H.; Sutcliffe, J.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 1696-1700, 1988
A;Title: Phenol emulsion-enhanced DNA-driven subtractive cDNA cloning: isolation of low-

Db	1	MLSCLQCALAALSIVLALGGVTGAPS DPLR
QY	61	AHVENEAIELDDMSHGVEQEDVDLEERA--
	61	NQTEIDALEPEDLSQLSQAEEQDEMRLELQRSAN
Db		
RESULT	8	
RIRTS1		
Somatostatin precursor		rat
N; Alternate names:		preprosomatostatin

A; Molecule type: mRNA
A; Residues: 1-116 <TRA>
A; Cross-references: GB: M19318; NID: g342298; PID: AAA36908.1; PID: g342299
C; Comment: Somatostatin inhibits the release of somatotropin.
C; Superfamily: somatostatin
C; Keywords: hormone; neuropeptide
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-88/Domain: propeptide #status predicted <PRO>
F; 89-116/Product: somatostatin-28 #status predicted <M28>
F; 103-116/Product: somatostatin-14 #status predicted <M14>
F; 105-116/Disulfide bonds: #status predicted

Species: *Agelaius phoeniceus* (norway lue)
 C; Date: 03-Aug-1984 #sequence_revision 03
 C; Accession: A20983; A01431; A47598; A225
 R; Montminy, M.R.; Goodman, R.H.; Horovitz
 Proc. Natl. Acad. Sci. U.S.A. 81, 3337-33
 A; Title: Primary structure of the gene en
 A; Reference number: A20983; MUID:84221954
 A; Accession: A20983
 A; Molecule type: DNA
 A; Residues: 1-116 <MON>
 A; Cross-references: GB:J00787; NID:q20702
 A; Note: the authors translated the codon
 B; Argos, P.; Taylor, W.H.; Minth, C.D.; i

A; Title: Nucleotide and amino acid sequence
A; Reference number: A01431; MUID:83238516
A; Accession: A01431
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-116 <ARG>
R; Benoit, R.; Ling, N.; Esch, F.
Science 238, 1126-1129, 1987
A; Title: A new pro somatostatin-derived peptide
A; Reference number: A47598; MUID:88070564
A; Accession: A47598

RESULT 7
RIBOS1
somatostatin precursor - bovine
N;Alternate names: preprosomatostatin
N;Contains: somatostatin 14 (SS-14); somatostatin 28 (SS-28)
C;Species: Bos primigenius taurus. (cattle)
C;Date: 06-Mar-1992 #sequence_revision 31-Jan-1997 #text_change 18-Jun-1999.
C;Accession: A40929
R;Su, C.J.; White, J.W.; Li, W.H.; Luo, C.C.; Frazier, M.L.; Saunders, G.F.;
Mol: Endocrinol. 2, 209-216, 1988
A;Title: Structure and evolution of somatostatin genes.

A; Source: PDB: 2JFC: PROCB
A; Residues: 25-34 <BEN>
R; Tavianini, M.A.; Hayes, T.E.; Magazin,
J. Biol. Chem. 259, 11798-11803, 1984
A; Title: Isolation, characterization, and
A; Reference number: A22529; MUID:85006903
A; Accession: A22529
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-116 <TAV>
A; Cross-references: GB:K02248; NID:q20701
R; Goodman, R.H.; Jacobs, J.W.;
Dee, P.C.;

J. Biol. Chem. 257, 1156-1159, 1982
 A; Title: Somatostatin-28 encoded in a cloned cDNA obtained from a rat medullary thyroid
 A; Reference number: I55220; MUID:82120034
 A; Accession: I55220
 A; Status: translated from GB/EMBL/DDBJ
 A; Molecule type: mRNA
 A; Residues: 38-78, 'H', 80-116 <RES>
 A; Cross-references: GB:J00788; PID:9207018; PID:AAA42162.1; PID:9207019
 R; Goodman, R.H.; Montanya, M.R.; Low, M.J.; Habener, J.F.
 Adv. Exp. Med. Biol. 188, 31-47, 1985
 A; Title: Biosynthesis of rat preprosomatostatin.
 A; Reference number: I51829; MUID:85303584
 A; Accession: I51829
 A; Status: translated from GB/EMBL/DDBJ
 A; Molecule type: mRNA
 A; Residues: 1-116 <RE2>
 A; Cross-references: GB:M25890; PID:9207030; PID:AAA42167.1; PID:9207031
 C; Comment: Somatostatins are found in a variety of tissues, including hypothalamus, cere
 C; Genetics: 4/6/3
 Function:
 Description: inhibits the secretion of a number of peptide hormones, including somatot
 C; Superfamily: somatostatin
 C; Keywords: hormone; hypothalamus; neuropeptide
 F; 1-24/Domain: signal sequence #status predicted <SIG>
 F; 25-88/Domain: propeptide #status experimental <PRO>
 F; 89-116/Product: somatostatin-28 #status predicted <S28>
 F; 103-116/Product: somatostatin-14 #status predicted <S14>
 F; 105-116/Disulfide bonds: #status predicted

Query Match 61.3%; Score 347; DB 1; Length 116;
 Best Local Similarity 59.5%; Pred. No. 3.9e-26;
 Matches 69; Conservative 17; Mismatches 28; Indels 2; Gaps 1;

Qy 1 MLSTRVQCALLLAIASSVAAAPSDAKIRQLLQRSLMAPAGKQELARNTLVELLSEL 60
 Db 1 MLSCLRQLCALAALCIVLALGGVTGAPS DPRQLQFLQSLAAATGQELAKYFLAELLSEP 60
 Qy 61 AHVNEAIELDDMSHGVQEDVDLLELERA - PGPVLAPRERKAGCKNFFWKTFTSC 114
 Db 61 NOTENDALEPEDLPQAAEQDEMRLQSLRANSNSPAMAPRERKAGCKNFFWKTFTSC 116

RESULT 9
 RIMSS1
 Somatostatin precursor - mouse
 N; Alternate names: preprosomatostatin
 Contains: somatostatin 14 (SS-14); somatostatin 28 (SS-28)
 C; Species: Mus musculus (house mouse)
 C; Date: 31-Dec-1990 #sequence_revision 31-Jan-1997 #text_change 18-Jun-1999
 C; Accession: S08416
 R; Fuhrmann, G.; Heilig, R.; Kempf, J.; Ebel, A.
 Nucleic Acids Res. 18, 1287, 1990
 A; Title: Nucleotide sequence of the mouse preprosomatostatin gene.
 A; Reference number: S08416; MUID:90206793
 A; Accession: S08416
 A; Molecule type: DNA
 A; Residues: 1-116 <FUH>
 A; Cross-references: EMBL:X51468; PID:953768; PID:CAA35831.1; PID:9297530
 C; Comment: Somatostatin inhibits the release of somatotropin.
 C; Genetics: 4/6/3
 C; Superfamily: somatostatin
 C; Keywords: hormone; neuropeptide
 F; 1-24/Domain: signal sequence #status predicted <SIG>
 F; 25-88/Domain: propeptide #status predicted <PRO>
 F; 89-116/Product: somatostatin-28 #status predicted <M28>
 F; 103-116/Product: somatostatin-14 #status predicted
 F; 105-116/Disulfide bonds: #status predicted

Query Match 61.3%; Score 347; DB 1; Length 116;

Best Local Similarity 59.5%; Pred. No. 3.9e-26;
 Matches 69; Conservative 17; Mismatches 28; Indels 2; Gaps 1;
 Qy 1 MLSTRVQCALLLAIASSVAAAPSDAKIRQLLQRSLMAPAGKQELARNTLVELLSEL 60
 Db 1 MLSCLRQLCALAALCIVLALGGVTGAPS DPRQLQFLQSLAAATGQELAKYFLAELLSEP 60
 Qy 61 AHVNEAIELDDMSHGVQEDVDLLELERA - PGPVLAPRERKAGCKNFFWKTFTSC 114
 Db 61 NOTENDALEPEDLPQAAEQDEMRLQSLRANSNSPAMAPRERKAGCKNFFWKTFTSC 116
 RESULT 10
 RIGPS
 Somatostatin I precursor - pig (fragment)
 N; Alternate names: prosomatostatin
 N; Contains: somatostatin 14 (SS-14); somatostatin 28 (SS-28)
 C; Species: Sus scrofa domestica (domestic pig)
 C; Date: 30-Nov-1980 #sequence_change 31-Jan-1997 #text_change 31-Jan-1997
 C; Accession: A34109; A24222; A91273; A93854; A90398; S13616; A01432
 R; Bersani, M.; Thim, L.; Baldissera, F.G.A.; Holst, J.J.
 J. Biol. Chem. 264, 10633-10636, 1989
 A; Title: Prosomatostatin 1-64 is a major product of somatostatin gene expression in F
 A; Reference number: A34109; MUID:89278131
 A; Accession: A34109
 A; Molecule type: protein
 A; Residues: 1-64 <BER>
 R; Schmidt, W.E.; Mutt, V.; Kratzin, H.; Carlquist, M.; Conlon, J.M.; Creutzfeldt, W.
 FEBS Lett. 192, 141-146, 1985
 A; Title: Isolation and characterization of proSS1-32, a peptide derived from the N-terminus
 A; Reference number: A24222; MUID:86030691
 A; Accession: A24222
 A; Molecule type: protein
 A; Residues: 1-32 <SC3>
 R; Pradayrol, L.; Jornvall, H.; Mutt, V.; Ribet, A.
 FEBS Lett. 109, 55-58, 1980
 A; Title: N-terminally extended somatostatin: the primary structure of somatostatin-28
 A; Reference number: A91273; MUID:80113258
 A; Accession: A91273
 A; Molecule type: protein
 A; Residues: 65-92 <PRA>
 A; Experimental source: intestine
 R; Schally, A.V.; Huang, W.Y.; Chang, R.C.C.; Arimura, A.; Redding, T.W.; Millar, R.P.
 Proc. Natl. Acad. Sci. U.S.A. 77, 4489-4493, 1980
 A; Title: Isolation and structure of pro-somatostatin: a putative somatostatin precursor
 A; Reference number: A93854; MUID:81054799
 A; Accession: A93854
 A; Molecule type: protein
 A; Residues: 65-92 <SC2>
 A; Experimental source: hypothalamus
 R; Bersani, M.; Johnson, A.H.; Holst, J.J.
 FEBS Lett. 279, 237-239, 1991
 A; Title: Oxidation/reduction explains heterogeneity of pancreatic somatostatin.
 A; Reference number: S13616; MUID:91160722
 A; Accession: S13616
 A; Molecule type: protein
 A; Residues: 79-92 <BE2>
 A; Comment: Somatostatin inhibits the release of somatotropin.
 C; Superfamily: somatostatin
 C; Keywords: hormone; hypothalamus; intestine; neuropeptide
 F; 1-64/Domain: propeptide #status experimental <PRO>
 F; 65-92/Product: somatostatin-28 #status experimental <M28>
 F; 79-92/Product: somatostatin-14 #status experimental <M14>
 F; 37/Binding site: carbohydrate (Asn) (covalent) #status absent
 F; 81-92/Disulfide bonds: #status experimental

C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C; Accession: I51064
 R; Moore, C.A.; Kittilson, J.D.; Dahl, S.K.; Sheridan, M.A.
 Gen. Comp. Endocrinol. 98, 253-261, 1995
 A; Title: Isolation and characterization of a cDNA encoding for preprosomatosstatin co-
 A; Reference number: I51064; MUID:95354921
 A; Accession: I51064
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-115 <MOO>
 A; Cross-references: EMBL:U32471; NID:9975344; PIDN: AAC59695.1; PID:9975345
 C; Superfamily: somatosstatin

Query Match 51.8%; Score 293; DB 1; Length 92;
 Best Local Similarity 63.0%; Pred. No. 4.3e-21;
 Matches 58; Conservative 13; Mismatches 19; Indels 2; Gaps 1;

Qy 25 APDAKLQLLRSIPLAPGKQELARNTLVELLSELAHVNNEAIELDDMSHGVQEDVLD 84
 Db 1 APSPDRPRQFLQSKLARRAGKQELAKYFLAELSEPNTENDALEPDLSQAREQDEMRL 60

Qy 85 ELERA--PGPVLAAPRERKAGCKNPFWKTFSTC 114
 Db 61 ELQRSANSNPAMAPRERKAGCKNPFWKTFSTC 92

RESULT 11
 RIAFS1
 somatosstatin I precursor - American goosefish
 N; Contains: somatosstatin I
 ; Species: *Lophius americanus* (American goosefish)
 ; Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 28-May-1999
 C; Accession: A93236; A93860; A91087; A01433
 R; Hobart, P.; Crawford, R.; Shen, L.; Pictet, R.; Rutter, W.J.
 Nature 288, 137-141, 1980
 A; Title: Cloning and sequence analysis of cDNAs encoding two distinct somatosstatin precu
 A; Reference number: A93236; MUID:81052423
 A; Accession: A93236
 A; Molecule type: mRNA
 A; Residues: 1-121 <HOB>
 A; Cross-references: GB:V00640; GB:J00946; PIDN:CAA23986.1; PID:964029
 R; Goodman, R.H.; Jacobs, J.W.; Chin, W.W.; Lund, P.K.; Dee, P.C.; Habener, J.F.
 Proc. Natl. Acad. Sci. U.S.A. 77, 5869-5873, 1980
 A; Title: Nucleotide sequence of a cloned structural gene coding for a precursor of pancreatic somatosstatin II precursor - American goosefish
 C; Species: *Lophius americanus* (American goosefish)
 C; Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 28-May-1999
 C; Accession: B93236; A94038; A27376; A01434; A21881; A93236
 R; Hobart, P.; Crawford, R.; Shen, L.; Pictet, R.; Rutter, W.J.
 Nature 288, 137-141, 1980
 A; Title: Cloning and sequence analysis of cDNAs encoding two distinct somatosstatin precursors
 A; Reference number: A93236; MUID:81052423
 A; Accession: A93236
 A; Molecule type: mRNA
 A; Residues: 1-125 <HOB>
 A; Cross-references: GB:V00641; GB:J00947; GB:M23199; PIDN:CAA23987.1; PID:964030
 R; Spiess, J.; Noe, B.D.; Proc. Natl. Acad. Sci. U.S.A. 82, 277-281, 1985
 A; Title: Processing of an anglerfish somatosstatin precursor, to a hydroxylysine-conta
 A; Reference number: A94038; MUID:85113184
 A; Accession: A94038
 A; Molecule type: protein
 A; Residues: 98-125 <SP1>
 R; Andrews, P.C.; Nichols, R.; Dixon, J.E.
 J. Biol. Chem. 262, 12692-12699, 1987
 A; Title: Post-translational processing of preprosomatosstatin-II examined using fast
 A; Reference number: A27376; MUID:87308304
 A; Accession: A27376
 A; Molecule type: protein
 A; Residues: 1-76 'DV' 79-89, 'G' 91-125 <AND>
 C; Superfamily: somatosstatin
 C; Keywords: hydropeptide; neuropeptide; pyroglutamic acid
 F; 1-24/Domain: signal sequence #status experimental <SIG>
 F; 25-97/Domain: propeptide #status experimental <PRO>
 F; 97-125/Product: somatosstatin II #status experimental <MAT>
 F; 25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
 F; 114-125/Disulfide bonds: #status experimental
 F; 120/Modified site: hydroxylysine (Lys) #status experimental

Query Match 28.7%; Score 162.5; DB 1; Length 125;
 Best Local Similarity 38.9%; Pred. No. 1.8e-08;
 Matches 51; Conservative 16; Mismatches 41; Indels 23; Gaps 6;

RESULT 12
 I51064
 somatosstatin II precursor - rainbow trout
 C; Species: *Oncorhynchus mykiss* (rainbow trout)

Query 1 MLSTRVQCALALLSLAIISSVSA-----APSDAKLRLQ--LLQRLSLMAPAGKQELA 49
 Database 1 MCICRCPAIALLVLVCGPSVSSQLDREQSDNQDLDLRLQRWLLERARSAGLSQLQEW 60

Query 50 RNTLVELLSEL---AHVNEAIELDDMSHGVQEDVLDLELERAPGV--LAPRERKAGC 103
 Database 61 RRAVEELLAQMSLPEATFQREA--EDASMATEGR--MLNERSVDSSTNNLPPRERKAGC 114

Query 104 KNFFWKTKTFRSC 114
 Database 115 RNFYWKRGFRSC 125

RESULT 14
 A61322 somatostatin-28 - sheep
 N;Contains: somatostatin-14
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
 Accession: A61322; A61344
 J;Spies, J.; Villarreal, J.; Vale, W.
 Biochemistry 20, 1982-1988, 1981
 A;Title: Isolation and sequence analysis of a somatostatin-like polypeptide from ovine
 A;Reference number: A61322; MUID:81184502
 A;Accession: A61322
 A;Molecule type: protein
 A;Residues: 1-28 <SP1>
 R;Burgus, R.; Ling, N.; Butcher, M.; Guillenain, R.
 PROC. NATL. ACAD. SCI. U.S.A. 70, 684-688, 1973
 A;Title: Primary structure of somatostatin, a hypothalamic peptide that inhibits the secretion of pitressin and vasopressin
 A;Reference number: A61322; MUID:73209562
 A;Accession: A61344
 A;Molecule type: protein
 A;Residues: 15-28 <BUR>
 C;Superfamily: somatostatin
 C;Keywords: neuropeptide
 F;1-28/Product: somatostatin-28 #status experimental <S28>
 F;15-28/Product: somatostatin-14 #status experimental <S14>
 F;17-28/Disulfide bonds: #status experimental

Query Match 22.4%; Score 127; DB 2; Length 28;
 Best Local Similarity 91.3%; Pred. No. 8e-06;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query 92 PVLPRAERKAGCKNFFWKTFTSC 114
 Database 6 PAMAPRERKAGCKNFFWKTFTSC 28

RESULT 15
 A32271 somatostatin-related protein - Atlantic hagfish
 C;Species: Myxine glutinosa (Atlantic hagfish)
 Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 31-Dec-1993
 C;Accession: A32271
 R;Conlon, J.M.; Asksten, U.; Falkmer, S.; Thim, L.
 Endocrinology 122, 1855-1859, 1988
 A;Title: Primary structures of somatostatins from the islet organ of the hagfish suggest
 A;Reference number: A32271; MUID:81195948
 A;Accession: A32271
 A;Molecule type: protein
 A;Residues: 1-34 <CON>
 C;Superfamily: somatostatin
 C;Keywords: neuropeptide

Query Match 20.6%; Score 116.5; DB 2; Length 34;
 Best Local Similarity 60.5%; Pred. No. 0.0001;
 Matches 23; Conservative 3; Mismatches 7; Indels 5; Gaps 1;

Query 77 VEQEDVDELELERAPGVLPRAERKAGCKNFFWKTFTSC 114

RESULT 2
 SMS1_ICTPU STANDARD; PRT; 114 AA.
 ID SMS1_ICTPU STANDARD; PRT; 114 AA.
 AC P01171;
 DT 21-JUL-1986 (Rel. 01; Created)
 DT 01-AUG-1990 (Rel. 15; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Somatostatin I precursor [Contains: Somatostatin-14].
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Siluriformes; Ictaluridae; Ictalurus.
 OX NCBI_TAXID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85303576; PubMed=2863931;
 RA DIXON J.E., Andrews P.C.;
 RT "Somatostatin of the channel catfish.";
 Adv. Exp. Med. Biol. 188:19-29(1985).
 AN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82265698; PubMed=6179939;
 RA Minth C.D., Taylor W.L., Magazin M.D., Tavianini M.A., Collier K.J.,
 Weith H.L., Dixon J.E.;
 RT "The structure of cloned DNA complementary to catfish pancreatic
 somatostatin-14 messenger RNA.";
 RT Proc. Natl. Acad. Sci. U.S.A. 78:6694-6698(1981).
 RL J. Biol. Chem. 257:10372-10377(1982).
 RN [3]
 RP SEQUENCE OF 82-114 FROM N.A.
 RX MEDLINE=82082515; PubMed=6171821;
 RA Taylor W.L., Collier K.J., Deschenes R.J., Weith H.L., Dixon J.E.;
 RT "Sequence analysis of a cDNA coding for a pancreatic precursor to
 somatostatin.";
 Proc. Natl. Acad. Sci. U.S.A. 78:6694-6698(1981).
 RN [4]
 RP SEQUENCE OF 101-114 FROM N.A.
 RX MEDLINE=81264223; PubMed=6114953;
 RA Andrews P.C., Dixon J.E.;
 RT "Isolation and structure of a peptide hormone predicted from a mRNA
 sequence. A second somatostatin from the catfish pancreas..";
 RL J. Biol. Chem. 256:8267-8270(1981).
 CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 CC -1-
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 CC -1-
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 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -1-
 DR EMBL; M25903; AAA49339.1; -;
 DR EMBL; V00607; CAA23877.1; -;
 DR V00608; CAA23878.1; -;
 DR PIR; S00292; RIIDS1; -;
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal;
 KW Multigene family.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 FT DISULFID 103 114 E -> O (IN REF. 2).
 FT CONFLICT 62 62 SEQUENCE 114 AA; 12419 MW; FEE0F2C76F74D99F CRC64;
 SQ

Matches 79; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

Query Match 72.3%; Score 409; DB 1; Length 114;
 Best Local Similarity 69.3%; Pred. No. 5.6e-32;

RESULT 3
 SMS1_CHICK STANDARD; PRT; 116 AA.
 ID SMS1_CHICK STANDARD; PRT; 116 AA.
 AC P33094;
 DT 01-OCT-1993 (Rel. 27; Created)
 DT 01-OCT-1993 (Rel. 27; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Somatostatin precursor [Contains: Somatostatin-14].
 GN SST
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TAXID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Nata K., Kobayashi T., Kato S., Yamamoto H.,
 RA Yonekura H., Okamoto H.;
 RL Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases.
 CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 CC -1-
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 or send an email to license@isb-sib.ch).
 CC -1-
 DR EMBL; X60191; CAA42747.1; -;
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT PROPEP 25 88 BY SIMILARITY.
 FT PEPTIDE 89 116 SOMATOSTATIN-28.
 FT PEPTIDE 103 116 SOMATOSTATIN-14.
 FT DISULFID 105 116 SQ SEQUENCE 116 AA; 12675 MW; 8A5BB9BDA8A291BA CRC64;
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT PROPEP 25 88 BY SIMILARITY.
 FT PEPTIDE 89 116 SOMATOSTATIN-28.
 FT PEPTIDE 103 116 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 103 114 E -> O (IN REF. 2).
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.
 FT PEPTIDE 101 114 SOMATOSTATIN-14.
 DR PIR; S20630; S20630;
 DR InterPro; IPR004250; Somatostatin;
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal.
 FT SIGNAL 1 24 PROBABLE.<

RT Intermediates.;"

RL Regul. Pept. 67:145-152(1996).

CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.

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CC DR EMBL; AF031488; AAC04697.1;

CC DR EMBL; Y15267; CAA75556.1;

CC DR InterPro; IPR004250; Somatostatin.

CC DR Pfam; PF03002; Somatostatin; 1.

CC KW Cleavage on pair of basic residues; Hormone; Signal.

CC FT SIGNAL 1 24 BY SIMILARITY.

CC FT PROPEP 25 88 BY SIMILARITY.

CC FT PEPTIDE 89 116 SOMATOSTATIN-28.

CC FT PEPTIDE 103 116 SOMATOSTATIN-14.

CC FT DISULFID 105 116 BY SIMILARITY.

CC SQ SEQUENCE 116 AA; 12689 MW; C18F17E31A3718DE CRC64;

Query Match 63.8%; Score 361; DB 1; Length 116;

Best Local Similarity 62.1%; Pred. No. 1.9e-27;

Matches 72; Conservative 17; Mismatches 25; Indels 2; Gaps 1;

Qy 1 MLSTRYQCALALLSALAISSSVAAAPSDAKIRQLLQLRSILMAPAGKQELARNTLVELLSEL 60

Db 1 MLSCRILQCALAALSIVIALGGVTCAQSPDPRUQFLQKSLLAAAGKQELAKYFLAELLSEP 60

Qy 61 AHVNEAIELDDMSHGVQEVDVDELEERA -PGPVLAQPRERKAGCKNFFWKTFSC 114

Db 61 NOTENDALEPEDLSQAAEQDEMRLELQRSANSNPAMAPRERKAGCKNFFWKTFSC 116

RESULT 7

SMS_HUMAN

ID . SMS_HUMAN

STANDARD; PRT; 116 AA.

AC P01166;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Somatostatin precursor [Contains: Somatostatin-14].

GN Homo sapiens (Human), and

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606, 9541;

RN [1].

RP SEQUENCE FROM N.A.

RC SPECIES=Human;

RX MEDLINE=84146798; PubMed=6142531;

RA Shen L.-P., Rutter W.J.;

RT "Sequence of the human somatostatin I gene.";

RL Science 224:168-171(1984).

RN [2].

RP SEQUENCE FROM N.A.

RC SPECIES=Human;

RX MEDLINE=83014931; PubMed=6126875;

RA Shen L.-P., Pictet R.L., Rutter W.J.;

RT "Human somatostatin I: sequence of the cDNA.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:4575-4579(1982).

RN [3].

RP SEQUENCE FROM N.A.

RC SPECIES=M. fascicularis;

RX MEDLINE=88144503; PubMed=2894033;

RA Travis G.H., Sutcliffe J.G.;

RT "Phenol emulsion-enhanced DNA-driven subtractive cDNA cloning: isolation of low-abundance monkey cortex-specific mRNAs.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:1696-1700(1988).

CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.

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or send an email to licensee@isb-sib.ch).

CC EMBL; M31217; AAA30744.1;
CC EMBL; U97077; AAB58056.1;
CC PIR; A40929; A40929;
CC InterPro; IPR004250; Somatostatin;
CC Pfam; PF03002; Somatostatin; 1.

CC Cleavage on pair of basic residues; Hormone; Signal.
CC SIGNAL 1 24 BY SIMILARITY.
CC PROPEP 25 88 BY SIMILARITY.
CC PEPTIDE 89 116 BY SIMILARITY.
CC PEPTIDE 1.03 116 BY SIMILARITY-14.
CC DISULFID 1.05 116 BY SIMILARITY.
CC SEQUENCE 116 AA; 12688 MW; C18F17E64A371D8E CRC64;

CC PROPEP 25 88 Score 352; DB 1; Length 116;
CC PEPTIDE 89 116 Best Local Similarity 61.2%; Pred. No. 1.3e-26;
CC PEPTIDE 103 116 Matches 71; Conservative 17; Mismatches 26; Indels 2; Gaps

CC SIGNAL 1 24 BY SIMILARITY.
CC PROPEP 25 88 BY SIMILARITY.
CC PEPTIDE 89 116 BY SIMILARITY.
CC PEPTIDE 1.03 116 BY SIMILARITY.
CC DISULFID 1.05 116 BY SIMILARITY.
CC SEQUENCE 116 AA; 12688 MW; C18F17E64A371D8E CRC64;

Query Match 62:2%; Score 352; DB 1; Length 116;
Best Local Similarity 61.2%; Pred. No. 1.3e-26;
Matches 71; Conservative 17; Mismatches 26; Indels 2; Gaps

QY 1 MLSTRVQCALALLSALAAISSVSAAPSDAKLROLQLQRSLMAPAGKQELARNTLVELLSEL 60
Db 1 MLSCLRQCALAALSLIVLALGGVTGAPSQDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEP 60

QY 1 AHVNEAIEELDDMSHGVEQEDVDLELERA--PGPVLAQPRERKAGCKNFFFWKTFFTSC 114
Db 1 NQTEIDALEPEDLSQAAEQDEMRLQELQRSANSPAMAPRERKAGCKNFFFWKTFFTSC 116

b RESULT 10
SMS_MOUSE STANDARD PRT; 116 AA.
ID SMS_MOUSE STANDARD PRT; 116 AA.
AC P01167; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

Y. 1 MLSTRVQCALALLSALAAISSVSAAPSDAKLROLQLQRSLMAPAGKQELARNTLVELLSEL 60
1 MLSCLRQCALAALSLIVLALGGVTGAPSQDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEP 60

61 AHVNEAIEELDDMSHGVEQEDVDLELERA--PGPVLAQPRERKAGCKNFFFWKTFFTSC 114
61 NQTEIDALEPEDLSQAAEQDEMRLQELQRSANSPAMAPRERKAGCKNFFFWKTFFTSC 116

RESULT 9
SMS_BOVIN STANDARD PRT; 116 AA.
D SMS_BOVIN STANDARD PRT; 116 AA.
D P26917; 01-AUG-1992 (Rel. 23, Created)
C 01-AUG-1992 (Rel. 23, Last sequence update)

b RESULT 9
SMS_BOVIN STANDARD PRT; 116 AA.
D SMS_BOVIN STANDARD PRT; 116 AA.
D P26917; 01-AUG-1992 (Rel. 23, Created)
C 01-AUG-1992 (Rel. 23, Last sequence update)

16 OCT-2001 (Rel. 40, Last annotation update)
Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].

S Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].

S Bos taurus (Bovine).
C Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
C Bovidae; Bovinae; Bos.
X NCBITaxID-9913; [1]

P SEQUENCE FROM N.A.
MEDLINE-88288237; PubMed-2899837;
Su C.J., White J.W., Li W.H., Luo C.C., Frazier M.L., Saunders G.F.,
Chan L.; [2]

A "Structure and evolution of somatostatin genes.";
Mol. Endocrinol. 2:209-216(1988).

N SEQUENCE FROM N.A.
MEDLINE-99198780; PubMed-10100681;
Furu L.M., Kazmer G.W., Strausbaugh L., Zinn S.A.; [2]

P SEQUENCE FROM N.A.
MEDLINE-83213516; PubMed-6133871;
RA Goodman R.H., Aron D.C., Roos B.A.; [3]

P SEQUENCE FROM N.A.
MEDLINE-85303584; PubMed-2863939;
RA Goodman R.H., Montminy M.R., Low M.J., Habener J.F.; [4]

RT "Nucleotide and amino acid sequence comparisons of preprosomatostatins";
J. Biol. Chem. 259:11798-11803(1984).
RN SEQUENCE FROM N.A.
RC SPECIES=Rat; RX MEDLINE-85006903; PubMed-6148343;
RA Tavianini M.A., Hayes T.E., Magazin M.D., Minth C.D., Dixon J.E.; [3]

RT "Isolation, characterization, and DNA sequence of the rat somatostatin gene";
J. Biol. Chem. 259:11798-11803(1984).
RN SEQUENCE FROM N.A.
RC SPECIES=Rat; RX MEDLINE-83238516; PubMed-6134734;
RA Argos P., Taylor W.L., Minth C.D., Dixon J.E.; [4]

RT "Nucleotide and amino acid sequence comparisons of preprosomatostatins";
J. Biol. Chem. 258:5570-5573(1983).
RN SEQUENCE FROM N.A.
RC SPECIES=Rat; RX MEDLINE-83213516; PubMed-6133871;
RA Goodman R.H., Aron D.C., Roos B.A.; [3]

RT "Rat pre-pro-somatostatin. Structure and processing by microsomal membranes";
J. Biol. Chem. 258:5570-5573(1983).
RN SEQUENCE FROM N.A.
RC SPECIES=Rat; RX MEDLINE-85303584; PubMed-2863939;
RA Goodman R.H., Montminy M.R., Low M.J., Habener J.F.; [4]

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DB	1	MLSCRQLQCALAALCIVLALGGVTGAPSDFRLRQFLQKSLAAATGKQELAKYFLAELLSEP 60				
RT		* Biosynthesis of rat preprosomatostatin.";				
RL		Adv. Exp. Med. Biol. 188:31-47(1985).				
RN	[5]	SEQUENCE FROM N.A.				
RC		SPECIES=Rat;				
RX		Medline=84221954; PubMed=6145156;				
RA		Montminy M.R., Goodman R.H., Horovitch S.J., Habener J.F.;				
RT		* Primary structure of the gene encoding rat preprosomatostatin.";				
RL		Proc. Natl. Acad. Sci. U.S.A. 81:3337-3340(1984).				
RN	[6]	SEQUENCE OF 38-116 FROM N.A.				
RP		SEQUENCE OF 25-34.				
RC		SPECIES=Rat; STRAIN=SPRAGUE-DAWLEY;				
RC		Medline=882120034; PubMed=6120163;				
RA		Goodman R.H., Jacobs J.W., Dee P.C., Habener J.F.;				
RT		* Somatostatin-28 encoded in a cloned cDNA obtained from a rat medullary thyroid carcinoma. ";				
RT		J. Biol. Chem. 257:1156-1159(1982).				
RL		SEQUENCE OF 38-116 FROM N.A.				
RP		SEQUENCE OF 25-34.				
RC		SPECIES=Rat; STRAIN=SPRAGUE-DAWLEY;				
RC		Medline=88070564; PubMed=2891188;				
A		"A new prosomatostatin-derived peptide reveals a pattern for prohormone cleavage at monobasic sites.";				
RT		RT		"A new prosomatostatin-derived peptide reveals a pattern for prohormone cleavage at monobasic sites.";		
RL		RT		RT		"A new prosomatostatin-derived peptide reveals a pattern for prohormone cleavage at monobasic sites.";
RN	[8]	SEQUENCE FROM N.A.				
RP		SEQUENCE=Mouse; TISSUE=Brain;				
RC		Medline=90206793; PubMed=1969620;				
RA		Fuhrmann G., Heilig R., Kempf J., Ebel A.;				
RT		"Nucleotide sequence of the mouse preprosomatostatin gene.";				
RL		Nucleic Acids Res. 18:1287-1287(1990).				
CC		-!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.				
CC		-!- SUBCELLULAR LOCATION: Secreted.				
CC		-!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.				
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC		DR		EMBL; K02248; AAA42161.1; -		
CC		DR		EMBL; V01271; CAA24579.1; -		
CC		DR		EMBL; J00787; AAA42164.1; -		
CC		DR		EMBL; M25890; AAA42167.1; -		
CC		DR		EMBL; J00788; AAA42162.1; -		
CC		DR		EMBL; X51468; CAA35831.1; -		
CC		DR		PIR; A20983; RIRTS1.		
CC		DR		PIR; S08416; S08416.		
CC		DR		MGD; MGI:98326; Smst..		
CC		DR		InterPro; IPR004250; Somatostatin.		
CC		DR		Pfam; PF03002; Somatostatin; 1.		
CC		KW		Cleavage on pair of basic residues; Hormone; Signal.		
CC		FT		SIGNAL 1 24 ANTRIN.		
CC		FT		PEPTIDE 25 34 ANTRIN.		
CC		FT		PROPEP 35 88 SOMATOSTATIN-28.		
CC		FT		PEPTIDE 89 116 SOMATOSTATIN-14.		
CC		FT		PEPTIDE 103 116 SOMATOSTATIN-14.		
CC		FT		DISULFID 105 116 T -> Y (IN REF. 5).		
CC		FT		CONFLICT 43 43 Q -> H (IN REF. 6).		
CC		FT		SEQUENCE 79 79 D48B5454C4490375 CRC64;		
CC		SQ		116 AA; 12745 MW;		

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CC or send an email to license@isb-sib.ch).

CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC FT PROTEIN; V00640; CAA23986.1; 7.
CC DR PIR; A01433; RIAFSI.
CC DR InterPro; IPR004250; Somatostatin.
CC DR Pfam; PF03002; Somatostatin; 1.
CC KW Cleavage on pair of basic residues; Hormone; Signal;
CC NON_TER 1
CC FT PROPEP 1 64 SOMATOSTATIN-28.
CC FT PEPTIDE 65 92 SOMATOSTATIN-14.
CC FT DISULFID 79 92
CC FT DISULFID 81 92
CC SQ SEQUENCE 92 AA; 10346 MW; 787CBEB82CFBBAE76 CRC64;

Query Match 51.8%; Score 293; DB 1; Length 92;
Best Local Similarity 63.0%; Pred. No. 3.7e-21;
Matches 58; Conservative 13; Mismatches 19; Indels 2; Gaps 1;

QY 25 APSDAKLRQLLQLRQLSMLAPAGKQELARNTLVEAIELDDMSHGVEQDVLD 84
Db 1 APSDPRLRLQFQKSLAAAGKQELAKYFLAELLSEPNQTNDALEPEDLSQAAEQDEMRL 60

QY 85 ELERA - PGPVLA
Db 61 ELQRSANSNPAMAPRERKAGCKNFEWKLTETSC 92

RESULT 12
SMS1_LOPAM
ID SMS1_LOPAM STANDARD PRT; 121 AA.
AC P01169;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin I precursor [Contains: Somatostatin-14];
OS Lophius americanus (American goosefish) (Anglerfish);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius;
OX NCBI_TAXID-8073;
RN SEQUENCE FROM N.A.
MEDLINE-81052423; PubMed-6107860;
A Hobart P.M., Crawford R., Shen L., Pictet R., Rutter W.J.;
RT "Cloning and sequence analysis of cDNAs encoding two distinct
RT somatostatin precursors found in the endocrine pancreas of
RT anglerfish."
RL Nature 288:137-141(1980).
RN [2]
RP SEQUENCE OF 2-121 FROM N.A.
RX MEDLINE-81077276; PubMed-6108560;
RA Goodman R.H., Jacobs J.W., Chin W.W., Lund P.K., Dee P.C.,
RA Habener J.F.;
RT "Nucleotide sequence of a cloned structural gene coding for a
RT precursor of pancreatic somatostatin."
RL Proc. Natl. Acad. Sci. U.S.A. 77:5869-5873(1980).
RN [3]
RP ERBatum.
RA Goodman R.H., Jacobs J.W., Chin W.W., Lund P.K., Dee P.C.,
RA Habener J.F.;
RL Proc. Natl. Acad. Sci. U.S.A. 79:1682-1682(1982).
RN [4]
RP SEQUENCE OF 108-121.
RX MEDLINE-80046482; PubMed-387385;
RA Noe B.D., Spiess J., Rivier J.E., Vale W.;
RT "Isolation and characterization of somatostatin from anglerfish
RT pancreatic islet."
RL Endocrinology 105:1410-1415(1979).

CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC FT PROTEIN; V00640; CAA23986.1; 7.
CC DR PIR; A01433; RIAFSI.
CC DR InterPro; IPR004250; Somatostatin.
CC DR Pfam; PF03002; Somatostatin; 1.
CC KW Cleavage on pair of basic residues; Hormone; Signal;
CC KW Multigene family.
CC FT SIGNAL 1 24 PROBABLE.
CC FT PROPEP 25 105
CC FT PEPTIDE 108 121 SOMATOSTATIN-14.
CC FT DISULFID 110 121
CC FT CONFLICT 21 21 A -> V (IN REF. 2).
CC FT CONFLICT 83 83 G -> E (IN REF. 2).
CC SQ SEQUENCE 121 AA; 13325 MW; D70C53DC7982095 CRC64;

Query Match 44.3%; Score 251; DB 1; Length 121;
Best Local Similarity 51.3%; Pred. No. 4.5e-17;
Matches 60; Conservative 15; Mismatches 36; Indels 6; Gaps 4;

QY 3 STRVOCALA-LLSLALAISSVSAAPSADAKLRQLLQLRQLSMLAPAGKQELARNTLVE-LLSEL 60
ID SMS2_ONCMTY STANDARD PRT; 115 AA.
AC Q91194;
DB 6 SSRRLRCIVLLVLLSITASISCFAGORDSKRLLLHRYPL-QGSKQDMTRSLAELLSSLDL 64

QY 61 AHVNEAIELDDM---SHGVEQEDVDELEERAPGVLPVLA
DB 65 LOGENEALEEEENPFLAEGGPEDAHADLERAASCGPPLA
DE 61 AHVNEAIELDDM---SHGVEQEDVDELEERAPGVLPVLA
DE [Tyr21,Gly24] somatostatin-28;
DE Somatostatin II precursor [Contains: [Tyr21,Gly24] somatostatin-28;
DE [Tyr7,Gly10] somatostatin-14].
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TAXID-8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95354921; PubMed-7628684;
RA Moore C.A., Kittlison J.D., Dahl S.K., Sheridan M.A.;
RT "Isolation and characterization of a cDNA encoding for a
RT proprosomatostatin containing [Tyr7, Gly10]-somatostatin-14 from the
RT endocrine pancreas of rainbow trout. Oncorhynchus mykiss."
RL Gen. Comp. Endocrinol. 98:253-261(1995).
CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).

CC EMBL; U32471; AAC59695.1; -

DR InterPro; IPR004250; Somatostatin.

DR PF03002; Somatostatin; 1.

KW Cleavage on pair of basic residues; Hormone; Signal; Hydroxylation;

KW Multigene family.

FT SIGNAL 1 18 POTENTIAL.

FT PROPEP 19 87 [TYR21, GLY24]SOMATOSTATIN-28 (POTENTIAL).

FT PEPTIDE 88 115 [TYR7, GLY10]SOMATOSTATIN-14.

FT PEPTIDE 102 115 BY SIMILARITY.

FT DISULFID 104 115 MW; 520595025FCA6D91 CRC64;

SQ SEQUENCE 115 AA; 12963 MW; 14052 MW; 5E14605D7B9A46FE CRC64;

Query Match 31.4%; Score 177.5; DB 1; Length 115;

Best Local Similarity 34.7%; Pred. No. 3.6e-10;

Matches 50; Conservative 9; Mismatches 18; Indels 67; Gaps 4;

Qy 5 RVQCALALLSALAISSVSAAPS---DAKLRQLLQLRSLLMA-----41

Db 5 RIHCALALLGLALAIQCSQGAASQPDLDLRSRLLQRARAIAAWPHRSQGVSERWRTFYPNCP 64

Qy 42 -----PAGKQELARNLTVELLSELAHNEAIELDDMSHGVQEDVVDLELERAPGP 92

Db 65 CLRPRKVKCPAG-----AKEDLVEELERSVGN 91

Qy 93 V--LAPRERKAGCKNNFWKTFPTSC 114

Db 92 PNNLPPRERKAGCKNFWKGETSC 115

RESULT '14

ID SMS2_LOPAM STANDARD; PRT; 125 AA.

AC P01170; Q91066; (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 12, Last sequence update)

DT 01-OCT-1989 (Rel. 40, Last annotation update)

DE Somatostatin II precursor [Contains: [Tyr7, Gly10]somatostatin-14].

OS Lophius americanus (American goosefish) (Anglerfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius; NCBITaxon=8073;

RN [1] SEQUENCE FROM N.A.; PubMed=6107860;

RX MEDLINE=81052423; PubMed=6107860;

RA Hobart P.M., Crawford R., Shen L., Pictet R., Rutter W.J.;

RT "Cloning and sequence analysis of cDNAs encoding two distinct somatostatin precursors found in the endocrine pancreas of anglerfish."; Nature 288:137-141(1980).

RN PARTIAL SEQUENCE, AND HYDROXYLATION.

RP MEDLINE=87308304; PubMed=2887572;

RA Andrews P.C., Nichols R., Dixon J.E.;

RT "Post-translational processing of preprosomatostatin-II examined using fast atom bombardment mass spectrometry."; J. Biol. Chem. 262:12692-12699(1987).

CC 1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.

CC 1- SUBCELLULAR LOCATION: Secreted.

CC 1- MISCELLANEOUS: SOMATOSTATIN II MAY HAVE A DIFFERENT DEGREE OF ACTIVITY OR A DIFFERENT TYPE OF TARGET CELL FROM SOMATOSTATIN I.

CC 1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.

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CC EMBL; V00641; CAA23987.1;

DR PIR; A01434; RIAFS2.

DR PIR; A27376; A27376.

DR InterPro; IPR004250; Somatostatin.

DR PF03002; Somatostatin; 1.

KW Cleavage on pair of basic residues; Hormone; Signal; Hydroxylation;

KW Multigene family.

FT SIGNAL 1 24 POTENTIAL.

FT PROPEP 25 109 [TYR7, GLY10]SOMATOSTATIN-14.

FT PEPTIDE 112 125 [TYR7, GLY10]SOMATOSTATIN-14.

FT DISULFID 114 125 HYDROXYLATION.

FT MOD_RES 120 120 DV -> TG (IN REF. 1).

FT CONFLICT 77 78 G -> E (IN REF. 1).

FT CONFLICT 90 90 G -> E (IN REF. 1).

SQ SEQUENCE 125 AA; 14052 MW; 5E14605D7B9A46FE CRC64;

Query Match 28.9%; Score 163.5; DB 1; Length 125;

Best Local Similarity 38.2%; Pred. No. 8.2e-09;

Matches 50; Conservative 17; Mismatches 41; Indels 23; Gaps 5;

Qy 1 MLSTRVOCALLSLLAIISSVSA-----APSDAKLRQ--LLQRSLLMAPAGQELA 49

Db 1 MQCIRCPIAILLLAVLQGPPSSQOLDREQSDNQDLDLRLQHWLLEARSAGLISQEWS 60

Qy 50 RNTLVEELSEL---AHVNEAIELDDMSHGVQEDVVDLELERAPGP--LAPRERKAGC 103

Db 61 KRAVEELLAQMSLPEADVQREADASMATGG-----RMNLERSVSDSTNNLPPRERKAGC 114

Qy 104 KNFFWKTFFTSC 114

Db 115 KNFYWKGFTSC 125

RESULT 15

ID SMS2_CARAU STANDARD; PRT; 120 AA.

AC Q9YGH4; Q9PTU2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Somatostatin II precursor [Contains: [Tyr21, Gly24]somatostatin-14].

DE [Tyr7, Gly10]somatostatin-14].

OS Carassius auratus (Goldfish);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cyprinidae; Cyprinidae; Carassius.

NCBI_TAXID=7957;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Lin X.-W., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "The expression of SRIF mRNA in the brain of goldfish."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "The expression of SRIF mRNA in the brain of goldfish."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

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RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

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RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

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RA Otto C.J., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

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RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

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RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

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RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

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RC TISSUE=Liver;

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RC TISSUE=Liver;

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RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

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RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

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RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

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RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

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RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Otto C.J., Peter R.E.;

RT "Cloning and characterization of cDNAs encoding preprosomatostatin-1 and -II from goldfish brain."; Submitted (JUN-1996) to the EMBL/GenBank/DDB

DR EMBL; AF025686; AAF15306.1;
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin; 1.
 KW Cleavage on pair of basic residues; Hormone; Signal; Multigene family.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 92 POTENTIAL.
 FT PEPTIDE 93 120 [TYR21, GLY24] SOMATOSTATIN-28.
 FT PEPTIDE 107 120 [TYR7, GLY10] SOMATOSTATIN-14.
 FT DISULFID 109 120 BY SIMILARITY.
 FT CONFLICT 51 51 Q -> RW (IN REF. 2)
 SQ SEQUENCE 120 AA; 13723 MW; 98957D68011A651A CRC64;

Query Match 27.0%; Score 153; DB 1; Length 120;
 Best Local Similarity 37.9%; Pred. No. 7.6e-08;
 Matches 44; Conservative 16; Mismatches 48; Indels 8; Gaps 3;
 QY 6 VQCALLALLSALAI-----SSVSAAPSDAKLROLLQRLSMLAPAGKQELARNTLVELLSEL 60
 b 6 LHCYLLALLGLSLVLGRCANSQLEPDLDERRHRLLQRASATGQATQDFTKRDVERKLSSLL 65
 QY 61 AHVNEAIELDDMSHGVQEVDVLELERA--PGPVLAAPRERKAGCKNFEWKTFSTSC 114
 Db 66 SIPMEMRE-RGLSMAGESEDLRLQERSAESSNQLPTVRKEGCKNFYWKGFTSC 120

Search completed: June 13, 2002, 12:29:53
 Job time: 445 sec

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OM protein - protein search, using sw model

Run on: June 13, 2002, 12:22:58 ; Search time 60.72 seconds
(without alignments)
324,793 Million cell updates/sec

Title: US-09-727-739B-3
Perfect score: 566
Sequence: 1 MLSTRVQCALALLSLALAI.....APRERKAGCKNFFWKTFFTSC 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_19:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
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RESULT 4
 ID Q90Y42 PRELIMINARY; PRT; 114 AA.
 AC Q90Y42; ID Q90Y42 PRELIMINARY; PRT; 114 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DE 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 OS Chitala chitala.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Notopteridae; Chitala.
 OX NCBI_TaxID=112163;
 RN SEQUENCE FROM N.A.
 RA Al-Mahrouki A.A., Irwin D.M., Youson J.H.;
 RT "Characterization of variant somatostatin cDNAs from several
 osteoglossomorphs: molecular identification and comparative
 analysis.";
 RT Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF292653; AAK97070.1;
 SQ SEQUENCE 114 AA; 12561 MW; 4E3C32F58E34F971 CRC64;
 Query Match 80.2%; Score 454; DB 13; Length 114;
 Best Local Similarity 79.8%; Pred. No. 1.3e-36;
 Matches 91; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 AC Q90Y42; ID Q90Y42 PRELIMINARY; PRT; 114 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DE 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 OS SOMATOSTATIN.
 ACipenser transmontanus (white sturgeon)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
 Acipenserinae; Acipenser.
 OX NCBI_TaxID=7904;
 RN SEQUENCE FROM N.A.
 RA Trabucchi M., Tostivint H., Lihrmann I., Sollars C., Vallarino M.,
 Dores R.M., Vaudry H.;
 RT "Polygenic expression of somatostatin in the sturgeon Acipenser
 transmontanus: molecular cloning and distribution of the mRNAs
 encoding two somatostatin precursors.";
 RT J. Comp. Neurol. 0:0-0(2001).
 DR EMBL; AF395849; AAL13248.1;
 SQ SEQUENCE 116 AA; 12616 MW; 72E0C3FF6C80650F CRC64;

RESULT 5
 ID Q90Y43 PRELIMINARY; PRT; 115 AA.
 AC Q90Y43; ID Q90Y43 PRELIMINARY; PRT; 115 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DE 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 OS PREPROSOMATOSTATIN.
 Osteoglossum bicirrhosum (silver arowana).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 Osteoglossiformes; Osteoglossidae; Osteoglossum.
 OX NCBI_TaxID=109271;
 RN SEQUENCE FROM N.A.
 RA Al-Mahrouki A.A., Irwin D.M., Youson J.H.;
 RT "Characterization of variant somatostatin cDNAs from several
 osteoglossomorphs: molecular identification and comparative
 analysis.";
 RT Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF292650; AAK97067.1;
 SQ SEQUENCE 115 AA; 12791 MW; D65FBD7C6F1E4E4D CRC64;

Query Match 35.6%; Score 201.5; DB 13; Length 115;
 Best Local Similarity 43.8%; Pred. No. 3.7e-12;
 Matches 49; Conservative 17; Mismatches 43; Indels 3; Gaps 3

Query Match 5 RVOCALLSLALIASSVSAAPS-DAKLRLQLLQLRSLSMAPAGKQELARNTLVELLSEL 60
 AC Q90Y43; ID Q90Y43 PRELIMINARY; PRT; 115 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DE 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 OS PREPROSOMATOSTATIN.
 Osteoglossum bicirrhosum (silver arowana).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 Osteoglossiformes; Osteoglossidae; Osteoglossum.
 OX NCBI_TaxID=109271;
 RN SEQUENCE FROM N.A.
 RA Al-Mahrouki A.A., Irwin D.M., Youson J.H.;
 RT "Characterization of variant somatostatin cDNAs from several
 osteoglossomorphs: molecular identification and comparative
 analysis.";
 RT Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF292650; AAK97067.1;
 SQ SEQUENCE 115 AA; 12791 MW; D65FBD7C6F1E4E4D CRC64;

Query Match 70.7%; Score 400; DB 13; Length 116;
 Best Local Similarity 69.8%; Pred. No. 2.2e-31;
 Matches 81; Conservative 14; Mismatches 19; Indels 2; Gaps 1;

Query Match 5 RVOCALLSLALIASSVSAAPS-DAKLRLQLLQLRSLSMAPAGKQELARNTLVELLSEL 60
 AC Q90Y43; ID Q90Y43 PRELIMINARY; PRT; 115 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DE 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 OS PREPROSOMATOSTATIN.
 Osteoglossum bicirrhosum (silver arowana).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 Osteoglossiformes; Osteoglossidae; Osteoglossum.
 OX NCBI_TaxID=109271;
 RN SEQUENCE FROM N.A.
 RA Trabucchi M., Tostivint H., Lihrmann I., Sollars C., Vallarino M.,
 Dores R.M., Vaudry H.;
 RT "Polygenic expression of somatostatin in the sturgeon Acipenser
 transmontanus: molecular cloning and distribution of the mRNAs
 encoding two somatostatin precursors.";
 RT J. Comp. Neurol. 0:0-0(2001).
 DR EMBL; AF395849; AAL13248.1;
 SQ SEQUENCE 116 AA; 12616 MW; 72E0C3FF6C80650F CRC64;

Query Match 64 ENEAIELDDMSHGVQEDVDLELERA--PGPVLA
 AC Q90Y43; ID Q90Y43 PRELIMINARY; PRT; 115 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DE 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 OS PREPROSOMATOSTATIN.
 Osteoglossum bicirrhosum (silver arowana).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 Osteoglossiformes; Osteoglossidae; Osteoglossum.
 OX NCBI_TaxID=109271;
 RN SEQUENCE FROM N.A.
 RA Al-Mahrouki A.A., Irwin D.M., Youson J.H.;
 RT "Characterization of variant somatostatin cDNAs from several
 osteoglossomorphs: molecular identification and comparative
 analysis.";
 RT Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF292650; AAK97067.1;
 SQ SEQUENCE 115 AA; 12791 MW; D65FBD7C6F1E4E4D CRC64;

Query Match 65 QGE-VPOGAVSAADEEEDVRVDLERSLELNLP
 AC Q90Y43; ID Q90Y43 PRELIMINARY; PRT; 115 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DE 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 OS PREPROSOMATOSTATIN.
 Osteoglossum bicirrhosum (silver arowana).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 Osteoglossiformes; Osteoglossidae; Osteoglossum.
 OX NCBI_TaxID=109271;
 RN SEQUENCE FROM N.A.
 RA Trabucchi M., Tostivint H., Lihrmann I., Sollars C., Vallarino M.,
 Dores R.M., Vaudry H.;
 RT "Polygenic expression of somatostatin in the sturgeon Acipenser
 transmontanus: molecular cloning and distribution of the mRNAs
 encoding two somatostatin precursors.";
 RT J. Comp. Neurol. 0:0-0(2001).
 DR EMBL; AF395849; AAL13248.1;
 SQ SEQUENCE 116 AA; 12616 MW; 72E0C3FF6C80650F CRC64;

Best Local Similarity 81.0%; Pred. No. 0.006; Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;		CHAIN 88 Score 105 CORTISTATIN; SEQUENCE 105 AA; 11061 MW; F0DCD40052AB8E95 CRC64;			
QY 94 LAPRERKAGCKNFFFWKTFSC 114 8 LPARERKAGCKNFWKGFSC 28	RESULT 10 Q9PRV0 PRELIMINARY; PRT; 25 AA.	Query Match 15.0%; Score 85; DB 11; Length 105; Best Local Similarity 53.6%; Pred. No. 0.64; Matches 15; Conservative 2; Mismatches 11; Indels 0; Gaps 0;	FT SQ		
Db	Q9PRV0; AC	Q9PRV0; 01-MAY-2000 (TREMBLrel. 13, Created) 01-MAY-2000 (TREMBLrel. 13, Last sequence update) 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DE SOMATOSTATIN-RELATED PEPTIDE. OS Anguilla japonica (Japanese eel). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae; Anguilla. NCBI_TAXID=7937; N SEQUENCE. MEDLINE=95053622; PubMed=7525832; gesaka T., Yano K., Yamasaki M., Nagashima K., Ando M., RT "Somatostatin-related peptides isolated from the eel gut: effects on ion and water absorption across the intestine of the seawater eel."; J. Exp. Biol. 188:205-216(1994). InterPro; IPR004250; Somatostatin. Pfam; PF03002; Somatostatin; 1. SEQUENCE 25 AA; 2860 MW; BFC672143A04A3F5 CRC64;	RESULT 12 Q63803 PRELIMINARY; PRT; 715 AA. ID Q63803; AC Q63803; DT 01-NOV-1996 (TREMBLrel. 01, Created) DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DE XLALPHAS PROTEIN. GN XLAS. OS Rattus norvegicus (Rat). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus. NCBI_TAXID=10116; RN [1] SEQUENCE FROM N.A. RP MEDLINE=95089824; PubMed=7997272; RX Kehlenbach R.H., Huttner W.B.; RA Kehlenbach R.H., Matthey J., Huttner W.B.; RT "XLas is a new type of G protein."; RN [1] Nature 372:804-809(1994). RN [2] SEQUENCE FROM N.A. RP RA Kehlenbach R.H., Huttner W.B.; RT "The XL-domain of rat XLas is encoded by a single exon." RN [3] "Two overlapping reading frames in a single exon encode interacting proteins - a novel way of gene usage." Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases. RN [3] SEQUENCE OF 1-367 FROM N.A. RC STRAIN=WISTAR; RA Wang Y.Z., Kehlenbach R.H., Huttner W.B.; RT "The XL-domain of rat XLas is encoded by a single exon." RN [3] Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. DR EMBL; X84047; CAC39211.1; DR EMBL; AF093569; ADD03032.1; HSSP; P04896; 1AZT. DR InterPro; IPR001019; Gprotein_alpha. DR Pfam; PF00503; G-alpha; 1. DR PRINTS; PR00318; GPROTEINA. DR SMART; SM00275; G-alpha; 1. SQ SEQUENCE 715 AA; 68F9AAAC18159896 CRC64;	Query Match 14.0%; Score 79.5; DB 11; Length 715; Best Local Similarity 30.1%; Pred. No. 20; Matches 40; Conservative 13; Mismatches 55; Indels 25; Gaps 7;	FT SQ
QY 97 RERKAGCKNFFFWKTFSC 114 8 RERKAGCKNFWKGFPTSC 25	RESULT 11 Q9R1P8 PRELIMINARY; PRT; 105 AA.	Query Match 15.4%; Score 87; DB 13; Length 25; Best Local Similarity 83.3%; Pred. No. 0.076; Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	FT SQ		
Db	Q9R1P8; AC	Q9R1P8; 01-MAY-2000 (TREMBLrel. 13, Created) 01-MAY-2000 (TREMBLrel. 13, Last sequence update) 01-DEC-2001 (TREMBLrel. 19, Last annotation update) PREPROCORTISTATIN. CORT. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TAXID=10090; RN SEQUENCE FROM N.A. RC STRAIN=129/SV; RX Calbet M., Guadano-Ferraz A., Spier A.D., Maj M., Sutcliffe J.G., Przewlocki R., de Lecea L.; "Cortistatin and somatostatin mRNAs are differentially regulated in response to kainate"; Brain Res. Mol. Brain Res. 72:55-64 (1999). [2] SEQUENCE FROM N.A. RC Calbet-Murillo M., de Lecea L.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF050156; ADD51127.1; DR MGD; MGI:109538; Cort. InterPro; IPR004250; Somatostatin. Pfam; PF03002; Somatostatin; 1.	Query Match 2 LSTRVOCALLSLALAISSVSAAPSDAKLR----QLLQRSLMAPA----GK 45 Best Local Similarity 30.1%; Pred. No. 20; Matches 40; Conservative 13; Mismatches 55; Indels 25; Gaps 7;	FT SQ	
QY 103 CKNFFFWKTFSC 114	RESULT 13 Q9R1P8; AC	Db	Db		
Db	286 PVRNFPARAFGSC 298	QY 103 CKNFFFWKTFSC 114	QY 103 CKNFFFWKTFSC 114		
QY 103 CKNFFFWKTFSC 114	RESULT 13 Q9R1P8; AC	Db	Db		

001392 PRELIMINARY; PRT; 376 AA.
 AC 001392; 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE UNC-76 (C01G10.11B PROTEIN).
 GN UNC-76 OR C01G10.11B.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderrinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97250552; PubMed=9096408;
 RA Bloom L., Horvitz H.R.;
 RT "The Caenorhabditis elegans gene unc-76 and its human homologs define a new gene family involved in axonal outgrowth and fasciculation.";
 PROC. NATL. ACAD. SCI. U.S.A. 94:3414-3419(1997).
 RN [2]
 P SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C.elegans*: A platform for investigating biology.";
 RT Science 282:2012-2018(1998).
 RL EMBL; U60059; AAC47518.1;
 DR EMBL; Z81030; CAC70075.1;
 DR EMBL; 42378 MW; D5C573662735D327 CRC64;
 SQ SEQUENCE 376 AA; 42378 MW; D5C573662735D327 CRC64;

Query Match 13.6%; Score 77; DB 5; Length 376;
 Best Local Similarity 33.8%; Pred. No. 17; Indels 8; Gaps 4;
 Matches 24; Conservative 18; Mismatches 21; Indels 8; Gaps 4;

Qy 20 SSVSAAPSDAKLRLQLLQRSLMAPAGKQELARNTLVELLSE---LAHVENEAIELDMSHG 76
 Db 227 SSIQSSDADIKLRS-AQALVSNPDNLQELSYSKLVTLCMEAEMOLIRVYNESL-VDELAH- 283

Qy 77 VEQEDVDELE 87
 Db 284 -RDELDYEKE 292

RESULT 15
 Q9BJ45 PRELIMINARY; PRT; 323 AA.
 ID Q9BJ45
 AC Q9BJ45;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 36.6 KDA PROTEIN.
 OS Leishmania major.
 OC Euglenozoa; Kinetoplastida; Trypanosomatida; Leishmania.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21256109; PubMed=11356515;
 RA Pedroza A.L., Ruiz J.C., Tosi L.R.O., Cruz A.K.;
 RT "Characterization of three chromosomal ends of Leishmania major reveals transcriptional activity across arrays of reiterated and unique sequences.";
 RT Mol. Biochem. Parasitol. 114:71-80(2001).
 RL EMBL; AF33905; AAK28283.1;
 KW Hypothetical protein.
 SQ SEQUENCE 323 AA; 36566 MW; 8C92C045309068DF CRC64;

Query Match 13.3%; Score 75; DB 5; Length 323;
 Best Local Similarity 30.8%; Pred. No. 122; Indels 10; Gaps 4;
 Matches 32; Conservative 14; Mismatches 48; Indels 10; Gaps 4;

Qy 20 SSVSAAPSDA--KLRLQLRSLMAPAGKQELARNTLVELL--SELAHVENAEIELDDMS 74
 Db 91 SSVRCASEDAYADPQLLIRNQKKGVAVLNKKLSQLARPSSYISHAQERRQRRNDLT 150

Qy 75 HGVEQEDVDELE 87
 Db 151 HAA-QELIDLEYERHQLNATARSFNTMSAFFGAAVKDMTAC 193

Search completed: June 13, 2002, 12:31:02
 Job time: 484 sec

001392 PRELIMINARY; PRT; 385 AA.
 AC 001392; 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 01, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
 DE UNC-76.
 GN UNC-76.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderrinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bloom L., Horvitz H.R.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Matthews L.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 7-385 FROM N.A.
 RX MEDLINE=97250552; PubMed=9096408;
 RA Bloom L., Horvitz H.R.;

